76091

Access DB# __________

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Nirmal S. Basi Examiner # : 74538 Date: 9/19/02
Art Unit: 1646 Phone Number 30 89435 Serial Number: 09/729920
Mail Box and Bldg/Room Location: CM1 10E17 Mail rm 10D19 Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

****

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Isolated Human Transporter Proteins, Nucleic acids

Inventors (please provide full names): Karl Guegler et al

Earliest Priority Filing Date: 9/19/2000

CRF

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Please search SEQ ID NO: 1, 2, 3 (143, 306 residues) Seq 3 cancelled, too large

commercial + interference databases + issued

RECEIVED SEP 19 2002 TECH/CHEM (STIC)

Thank you

RUSH

****

STAFF USE ONLY		Type of Search		Vendors and cost where applicable	
Searcher:	D. Schreiber	NA Sequence (#)	1	STN	
Searcher Phone #:	308-4292	AA Sequence (#)	1	Dialog	
Searcher Location:	CM1 6A03	Structure (#)		Questel/Orbit	
Date Searcher Picked Up:	9/20	Bibliographic		Dr.Link	
Date Completed:	9/23	Litigation		Lexis/Nexis	
Searcher Prep & Review Time:	15	Fulltext		Sequence Systems	Compugen
Clerical Prep Time:		Patent Family		WWW/Internet	
Online Time:	6	Other		Other (specify)	

PTO-1590 (8-01)

FILE 'MEDLINE' ENTERED
FILE 'JAPIO' ENTERED
FILE 'BIOSIS'
FILE 'SCISEARCH'
FILE 'WPIDS'
FILE 'CAPLUS'
FILE 'EMBASE'
=> potassium channel and trek
L1 217 POTASSIUM CHANNEL AND TREK

=> dup rem l1
PROCESSING COMPLETED FOR L1
L2 73 DUP REM L1 (144 DUPLICATES REMOVED)

=> d ibib l2 1-73

L2 ANSWER 1 OF 73 MEDLINE
ACCESSION NUMBER: 2002165854 MEDLINE
DOCUMENT NUMBER: 21896085 PubMed ID: 11897836
TITLE: The ***TREK*** two P domain K+ channels.
COMMENT: Comment on: J Physiol. 2002 Mar 15;539(Pt 3):657-68
AUTHOR: Patel Amanda; Honore Eric
CORPORATE SOURCE: IPMC-CNRS, 660 Route des Lucioles, Sophia Antipolis, 06560
Valbonne, France.
SOURCE: JOURNAL OF PHYSIOLOGY, (2002 Mar 15) 539 (Pt 3) 647.
Journal code: 0266262. ISSN: 0022-3751.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Commentary
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200206
ENTRY DATE: Entered STN: 20020319
Last Updated on STN: 20020621
Entered Medline: 20020620

L2 ANSWER 2 OF 73 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 2002266838 MEDLINE
DOCUMENT NUMBER: 22001365 PubMed ID: 11886861
TITLE: Modulation of TASK-1 (Kcnk3) and TASK-3 (Kcnk9) ***potassium*** ***channels*** : volatile anesthetics and neurotransmitters share a molecular site of action.
AUTHOR: Talley Edmund M; Bayliss Douglas A
CORPORATE SOURCE: Department of Pharmacology, University of Virginia,
Charlottesville, Virginia 22908-0735, USA..
emt3m@virginia.edu
CONTRACT NUMBER: NS33583 (NINDS)
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2002 May 17) 277 (20)
17733-42.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF031384; GENBANK-AF391084
ENTRY MONTH: 200207
ENTRY DATE: Entered STN: 20020514
Last Updated on STN: 20020717
Entered Medline: 20020716

L2 ANSWER 3 OF 73 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 2002322564 MEDLINE
DOCUMENT NUMBER: 22060496 PubMed ID: 12065410
TITLE: An intracellular proton sensor commands lipid- and mechano-gating of the K(+) channel ***TREK*** -1.
AUTHOR: Honore Eric; Maingret Francois; Lazdunski Michel; Patel
Amanda Jane
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire,
CNRS-UMR 6097, 660 route des Lucioles, Sophia Antipolis, F-06560 Valbonne, France.
SOURCE: EMBO JOURNAL, (2002 Jun 17) 21 (12) 2968-76.
Journal code: 8208664. ISSN: 0261-4189.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200208
ENTRY DATE: Entered STN: 20020615
Last Updated on STN: 20020830
Entered Medline: 20020829

L2 ANSWER 4 OF 73 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 2002238785 MEDLINE
DOCUMENT NUMBER: 21972941 PubMed ID: 11976378
TITLE: Long-term alteration of S-type potassium current and passive membrane properties in aplysia sensory neurons following axotomy.
AUTHOR: Ungless Mark A; Gasull Xavier; Walters Edgar T
CORPORATE SOURCE: Department of Integrative Biology and Pharmacology,
University of Texas-Houston Medical School, Houston, Texas
77030, USA.
CONTRACT NUMBER: NS-35882 (NINDS)
NS-35979 (NINDS)
RR-10294 (NCRR)
SOURCE: JOURNAL OF NEUROPHYSIOLOGY, (2002 May) 87 (5) 2408-20.
Journal code: 0375404. ISSN: 0022-3077.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Space Life Sciences
ENTRY MONTH: 200206
ENTRY DATE: Entered STN: 20020429
Last Updated on STN: 20020824
Entered Medline: 20020628

L2 ANSWER 5 OF 73 MEDLINE DUPLICATE 4
ACCESSION NUMBER: 2002191200 MEDLINE
DOCUMENT NUMBER: 21896087 PubMed ID: 11897838
TITLE: Expression pattern and functional characteristics of two novel splice variants of the two-pore-domain ***potassium*** ***channel*** ***TREK*** -2.
COMMENT: Comment in: J Physiol. 2002 Mar 15;539(Pt 3):647
AUTHOR: Gu Wenli; Schlichthorl Gunter; Hirsch Jochen R; Engels
Hartmut; Karschin Christine; Karschin Andreas; Derst Christian; Steinlein Ortrud K; Daut Jurgen
CORPORATE SOURCE: Institut fur Humangenetik, Universitat Bonn, Wilhelmstrasse
31, D-53111 Bonn, Germany.
SOURCE: JOURNAL OF PHYSIOLOGY, (2002 Mar 15) 539 (Pt 3) 657-68.
Journal code: 0266262. ISSN: 0022-3751.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200206
ENTRY DATE: Entered STN: 20020403
Last Updated on STN: 20020621
Entered Medline: 20020620

L2 ANSWER 6 OF 73 CAPLUS COPYRIGHT 2002 ACS
DUPLICATE 5
ACCESSION NUMBER: 2002:322996 CAPLUS
DOCUMENT NUMBER: 137:43030
TITLE: The ***TREK*** two P domain K+ channels
AUTHOR(S): Patel, Amanda; Honore, Eric
CORPORATE SOURCE: IPMC-CNRS, Valbonne, 06560, Fr.
SOURCE: Journal of Physiology (Cambridge, United Kingdom) (2002), 539(3), 647
CODEN: JPHYA7; ISSN: 0022-3751
PUBLISHER: Cambridge University Press
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
REFERENCE COUNT: 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 7 OF 73 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:365502 BIOSIS
DOCUMENT NUMBER: PREV200200365502
TITLE: Several tandem-pore K+ channels contribute to background K+
current in cerebellar granule neurons.
AUTHOR(S): Han, Jaehee (1); Truell, Jeffrey (1); Gnatenco, Carmen (1);
Kim, Donghee (1)
CORPORATE SOURCE: (1) Chicago Medical School, Chicago USA
SOURCE: Biophysical Journal, (January, 2002) Vol. 82, No. 1 Part 2,
pp. 636a. http://intl.biophysj.org/. print.
Meeting Info.: 46th Annual Meeting of the Biophysical Society San Francisco, California, USA February 23-27, 2002
ISSN: 0006-3495.
DOCUMENT TYPE: Conference
LANGUAGE: English

L2 ANSWER 8 OF 73 MEDLINE DUPLICATE 6
ACCESSION NUMBER: 2002376647 IN-PROCESS
DOCUMENT NUMBER: 22117977 PubMed ID: 12122143
TITLE: Characterization of four types of background ***potassium*** ***channels*** in rat cerebellar granule neurons.
AUTHOR: Han Jaehee; Truell Jeffrey; Gnatenco Carmen; Kim Donghee
CORPORATE SOURCE: Department of Physiology, Gyeongsang National University
School of Medicine, Chinju, Korea.
SOURCE: JOURNAL OF PHYSIOLOGY, (2002 Jul 15) 542 (Pt 2) 431-44.
Journal code: 0266262. ISSN: 0022-3751.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020718
Last Updated on STN: 20020718

L2 ANSWER 9 OF 73 MEDLINE
ACCESSION NUMBER: 2002309957 MEDLINE
DOCUMENT NUMBER: 22047240 PubMed ID: 12051718
TITLE: Validation of a quantitative method for real time PCR kinetics.
AUTHOR: Liu Weihong; Saint David A
CORPORATE SOURCE: Department of Physiology, University of Adelaide, Adelaide,
SA 5005, Australia.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2002
Jun 7) 294 (2) 347-53.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
(VALIDATION STUDIES)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200207
ENTRY DATE: Entered STN: 20020611
Last Updated on STN: 20020717
Entered Medline: 20020716

L2 ANSWER 10 OF 73 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:363310 BIOSIS
DOCUMENT NUMBER: PREV200200363310
TITLE: Expression pattern and functional characteristics of two novel splice variants of the two-pore-domain ***potassium*** ***channel*** ***TREK*** -2.
AUTHOR(S): Gu, W. (1); Schlichthoerl, G. (1); Hirsch, J. R. (1); Engels, H. (1); Karschin, C. (1); Karschin, A. (1); Derst, C. (1); Daut, J. (1)
CORPORATE SOURCE: (1) Institut fuer Normale und Pathologische Physiologie,
Universitaet Marburg, Deutschhausstrasse 2, 35037, Marburg Germany
SOURCE: Pfluegers Archiv European Journal of Physiology, (March,
2002) Vol. 443, No. Supplement 1, pp. S341.
http://link.springer.de/link/service/journals/00424/.
print.
Meeting Info.: 81st Annual Joint Meeting of the Physiological Society, the Scandinavian Physiological Society and the German Physiological Society Tuebingen, Germany March 15-19, 2002
ISSN: 0031-6768.
DOCUMENT TYPE: Conference
LANGUAGE: English

L2 ANSWER 11 OF 73 MEDLINE DUPLICATE 7
ACCESSION NUMBER: 2002174336 MEDLINE
DOCUMENT NUMBER: 21903759 PubMed ID: 11906167
TITLE: Molecular basis of the voltage-dependent gating of ***TREK*** -1, a mechano-sensitive K(+) channel.
AUTHOR: Maingret Francois; Honore Eric; Lazdunski Michel; Patel
Amanda Jane
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire, CNRS,
UMR 6097, Sophia Antipolis, Valbonne, France.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2002
Mar 29) 292 (2) 339-46.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200205
ENTRY DATE: Entered STN: 20020322
Last Updated on STN: 20020507
Entered Medline: 20020506

L2 ANSWER 12 OF 73 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 2002372279 EMBASE
TITLE: Background ***potassium*** ***channels*** move into
focus.
AUTHOR: Mathie A.; Clarke C.E.
CORPORATE SOURCE: A. Mathie, Biophysics Section, Blackett Laboratory,
Department of Biological Sciences, Prince Consort Road, London SW7 2BW, United Kingdom. a.mathie@ic.ac.uk
SOURCE: Journal of Physiology, (15 Jul 2002) 542/2 (334).
Refs: 7
ISSN: 0022-3751 CODEN: JPHYA7
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 002 Physiology
008 Neurology and Neurosurgery
LANGUAGE: English

L2 ANSWER 13 OF 73 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:387362 BIOSIS
DOCUMENT NUMBER: PREV200200387362
TITLE: Identification of twin-pore ***potassium*** ***channels*** in rat mesenteric arteries.
AUTHOR(S): Gardener, M. J. (1); Burnham, M. P. (1); Gilling, K. E.
(1); Johnson, I. T. (1); Edwards, G. (1); Weston, A. H. (1)
CORPORATE SOURCE: (1) School of Biological Sciences, University of
Manchester, Oxford Road, G.38 Stopford Building, Manchester, M13 9PT UK
SOURCE: British Journal of Pharmacology, (March, 2002) Vol. 135,
No. Proceedings Supplement, pp. 307P.
http://www.brjpharmacol.org/. print.

Meeting Info.: Meeting of the British Pharmacological Society London, England, UK December 17-21, 2001
ISSN: 0007-1188.
DOCUMENT TYPE: Conference
LANGUAGE: English

L2 ANSWER 14 OF 73 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:387339 BIOSIS
DOCUMENT NUMBER: PREV200200387339
TITLE: Twin-pore domain ***potassium*** ***channels*** in
rat pulmonary artery: Potential candidates of hypoxic pulmonary vasoconstriction.
AUTHOR(S): Johnson, I. T. (1); Gardener, M. J. (1); Richards, G. (1);
Burnham, M. (1); Glen, C. D. (1); Edwards, G. (1); Weston, A. H. (1)
CORPORATE SOURCE: (1) School of Biological Sciences, University of
Manchester, Oxford Road, G38 Stopford Building, Manchester,
M13 9PT UK
SOURCE: British Journal of Pharmacology, (March, 2002) Vol. 135,
No. Proceedings Supplement, pp. 284P.
http://www.brjpharmacol.org/. print.
Meeting Info.: Meeting of the British Pharmacological Society London, England, UK December 17-21, 2001
ISSN: 0007-1188.
DOCUMENT TYPE: Conference
LANGUAGE: English

L2 ANSWER 15 OF 73 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:322118 BIOSIS
DOCUMENT NUMBER: PREV200200322118
TITLE: Functional expression of ***TREK*** -2 K+ channel in cultured rat brain astrocytes.
AUTHOR(S): Gnatenco, Carmen (1); Kim, Donghee
CORPORATE SOURCE: (1) Chicago Medical School, 3333 Green Bay Road, North
Chicago, IL, 60064 USA
SOURCE: Biophysical Journal, (January, 2002) Vol. 82, No. 1 Part 2,
pp. 270a. http://intl.biophysj.org/. print.
Meeting Info.: 46th Annual Meeting of the Biophysical Society San Francisco, California, USA February 23-27, 2002
ISSN: 0006-3495.
DOCUMENT TYPE: Conference
LANGUAGE: English

L2 ANSWER 16 OF 73 MEDLINE DUPLICATE 8
ACCESSION NUMBER: 2002159167 MEDLINE
DOCUMENT NUMBER: 21888939 PubMed ID: 11891578
TITLE: ***Trek*** -like ***potassium*** ***channels***
in rat cardiac ventricular myocytes are activated by intracellular ATP.
AUTHOR: Tan J H C; Liu W; Saint D A
CORPORATE SOURCE: Cellular Biophysics Laboratory, The Department of
Physiology, University of Adelaide, Adelaide SA 5005, Australia.
SOURCE: JOURNAL OF MEMBRANE BIOLOGY, (2002 Feb 1) 185 (3) 201-7.
Journal code: 0211301. ISSN: 0022-2631.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200207
ENTRY DATE: Entered STN: 20020314
Last Updated on STN: 20020713
Entered Medline: 20020712

L2 ANSWER 17 OF 73 MEDLINE DUPLICATE 9
ACCESSION NUMBER: 2002165318 MEDLINE
DOCUMENT NUMBER: 21895240 PubMed ID: 11897089
TITLE: Functional expression of ***TREK*** -2 K+ channel in cultured rat brain astrocytes.
AUTHOR: Gnatenco Carmen; Han Jaehee; Snyder Ann K; Kim Donghee
CORPORATE SOURCE: Department of Physiology and Biophysics, Finch University
of Health Sciences/The Chicago Medical School, 3333 Green Bay Road, North Chicago, IL 60064-3095, USA.
SOURCE: BRAIN RESEARCH, (2002 Mar 22) 931 (1) 56-67.
Journal code: 0045503. ISSN: 0006-8993.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200205
ENTRY DATE: Entered STN: 20020319
Last Updated on STN: 20020522
Entered Medline: 20020520

L2 ANSWER 18 OF 73 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2002:113616 CAPLUS
DOCUMENT NUMBER: 137:104322
TITLE: A New Quantitative Method of Real Time Reverse Transcription Polymerase Chain Reaction Assay Based on Simulation of Polymerase Chain Reaction Kinetics
AUTHOR(S): Liu, Weihong; Saint, David A.
CORPORATE SOURCE: Department of Physiology, University of Adelaide,
Adelaide, 5005, Australia
SOURCE: Analytical Biochemistry (2002), 302(1), 52-59
CODEN: ANBCA2; ISSN: 0003-2697
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 19 OF 73 MEDLINE
ACCESSION NUMBER: 2001231249 MEDLINE
DOCUMENT NUMBER: 21219392 PubMed ID: 11319549
TITLE: Beam me up, Scottie! ***TREK*** channels swing both
ways.
COMMENT: Comment on: Nat Neurosci. 2001 May;4(5):486-91
AUTHOR: Maylie J; Adelman J P
SOURCE: NATURE NEUROSCIENCE, (2001 May) 4 (5) 457-8.
Journal code: 9809671. ISSN: 1097-6256.
PUB. COUNTRY: United States
DOCUMENT TYPE: Commentary
News Announcement
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200105
ENTRY DATE: Entered STN: 20010529
Last Updated on STN: 20010529
Entered Medline: 20010524

L2 ANSWER 20 OF 73 MEDLINE DUPLICATE 10
ACCESSION NUMBER: 2001667665 MEDLINE
DOCUMENT NUMBER: 21570223 PubMed ID: 11560940
TITLE: ***TREK*** -1 regulation by nitric oxide and cGMP-dependent protein kinase. An essential role in smooth muscle inhibitory neurotransmission.
AUTHOR: Koh S D; Monaghan K; Sergeant G P; Ro S; Walker R L;
Sanders K M; Horowitz B
CORPORATE SOURCE: Department of Physiology and Cell Biology, University of
Nevada School of Medicine, Reno, Nevada 89557, USA.
CONTRACT NUMBER: DK 41315 (NIDDK)
HL 49254 (NHLBI)
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2001 Nov 23) 276 (47)
44338-46.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200112
ENTRY DATE: Entered STN: 20011120
Last Updated on STN: 20020123
Entered Medline: 20011220

L2 ANSWER 21 OF 73 MEDLINE DUPLICATE 11
ACCESSION NUMBER: 2001520013 MEDLINE
DOCUMENT NUMBER: 21450949 PubMed ID: 11567039
TITLE: Cns distribution of members of the two-pore-domain (KCNK)
potassium ***channel*** family.
AUTHOR: Talley E M; Solorzano G; Lei Q; Kim D; Bayliss D A
CORPORATE SOURCE: Department of Pharmacology, University of Virginia,
Charlottesville, Virginia 22908, USA.. emt3m@virginia.edu
CONTRACT NUMBER: MH12091 (NIMH)
NS33583 (NINDS)
SOURCE: JOURNAL OF NEUROSCIENCE, (2001 Oct 1) 21 (19) 7491-505.
Journal code: 8102140. ISSN: 1529-2401.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200110
ENTRY DATE: Entered STN: 20010924
Last Updated on STN: 20011015
Entered Medline: 20011011

L2 ANSWER 22 OF 73 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 2001:240967 SCISEARCH
THE GENUINE ARTICLE: 410MC
TITLE: THIK-1 and THIK-2, a novel subfamily of tandem pore domain
K+ channels
AUTHOR: Rajan S; Wischmeyer E; Karschin C; Preisig-Muller R; Grzeschik K H; Daut J; Karschin A (Reprint); Derst C
CORPORATE SOURCE: Univ Marburg, Inst Humangenet, D-35032 Marburg, Germany
(Reprint); Univ Marburg, Inst Normal & Pathol Physiol, D-35032 Marburg, Germany; Max Planck Inst Biophys Chem,
D-37070 Gottingen, Germany
COUNTRY OF AUTHOR: Germany
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (9 MAR 2001) Vol. 276,
No. 10, pp. 7302-7311.
Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC,
9650 ROCKVILLE PIKE, BETHESDA, MD 20814 USA.
ISSN: 0021-9258.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 32
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L2 ANSWER 23 OF 73 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:562734 BIOSIS
DOCUMENT NUMBER: PREV200100562734
TITLE: SB-209712, a submicromolar inhibitor of ***TREK*** -1
potassium ***channels*** .
AUTHOR(S): Meadows, H. J. (1); Ray, A. M. (1); Heath, J. (1); Gager,
T. (1); Leslie, R. A. (1); Randall, A. D. (1)
CORPORATE SOURCE: (1) Neuroscience Research, GlaxoSmithKline, Harlow UK
SOURCE: Society for Neuroscience Abstracts, (2001) Vol. 27, No. 2,
pp. 1864. print.
Meeting Info.: 31st Annual Meeting of the Society for Neuroscience San Diego, California, USA November 10-15, 2001
ISSN: 0190-5295.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L2 ANSWER 24 OF 73 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:562721 BIOSIS
DOCUMENT NUMBER: PREV200100562721
TITLE: CNS distribution of members of the two-pore-domain (KCNK)
potassium ***channel*** family.
AUTHOR(S): Talley, E. M. (1); Solorzano, G. (1); Lei, Q. (1); Kim, D.;
Bayliss, D. A. (1)
CORPORATE SOURCE: (1) Dept. Pharmacol., Univ. of Virginia, Charlottesville,
VA USA
SOURCE: Society for Neuroscience Abstracts, (2001) Vol. 27, No. 2,
pp. 1862. print.
Meeting Info.: 31st Annual Meeting of the Society for Neuroscience San Diego, California, USA November 10-15, 2001
ISSN: 0190-5295.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L2 ANSWER 25 OF 73 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 2001:797985 SCISEARCH
THE GENUINE ARTICLE: 479JU
TITLE: Anesthetic-sensitive 2P domain K+ channels
AUTHOR: Patel A J; Honore E (Reprint)
CORPORATE SOURCE: Inst Pharmacol Mol & Cellulaire, CNRS UMR6097, 600 Route
Lucioles, F-06560 Valbonne, France (Reprint); Inst Pharmacol Mol & Cellulaire, CNRS UMR6097, F-06560 Valbonne, France
COUNTRY OF AUTHOR: France
SOURCE: ANESTHESIOLOGY, (OCT 2001) Vol. 95, No. 4, pp. 1013-1021.
Publisher: LIPPINCOTT WILLIAMS & WILKINS, 530 WALNUT ST,
PHILADELPHIA, PA 19106-3621 USA.
ISSN: 0003-3022.
DOCUMENT TYPE: General Review; Journal
LANGUAGE: English
REFERENCE COUNT: 67

L2 ANSWER 26 OF 73 MEDLINE DUPLICATE 12
ACCESSION NUMBER: 2001572938 MEDLINE
DOCUMENT NUMBER: 21535328 PubMed ID: 11680629
TITLE: Localization of ***TREK*** -2 K+ channel domains that
regulate channel kinetics and sensitivity to pressure, fatty acids and pHi.
AUTHOR: Kim Y; Gnatenco C; Bang H; Kim D
CORPORATE SOURCE: Department of Physiology and Biophysics, Finch University
of Health Sciences, The Chicago Medical School, IL 60064, USA.. donghee.kim@finchcms.edu
SOURCE: PFLUGERS ARCHIV. EUROPEAN JOURNAL OF PHYSIOLOGY, (2001 Sep)
442 (6) 952-60.
Journal code: 0154720. ISSN: 0031-6768.
PUB. COUNTRY: Germany: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200202
ENTRY DATE: Entered STN: 20011030
Last Updated on STN: 20020222
Entered Medline: 20020221

L2 ANSWER 27 OF 73 MEDLINE DUPLICATE 13

ACCESSION NUMBER: 2001370005 MEDLINE
DOCUMENT NUMBER: 21198116 PubMed ID: 11301200
TITLE: Distribution and expression of ***TREK*** -1, a two-pore-domain ***potassium*** ***channel*** , in the adult rat CNS.
AUTHOR: Hervieu G J; Cluderay J E; Gray C W; Green P J; Ranson J L;
Randall A D; Meadows H J
CORPORATE SOURCE: Neuroscience Research, SmithKline Beecham Pharmaceuticals,
Third Avenue, Essex CM19 5AW, Harlow, UK.
SOURCE: NEUROSCIENCE, (2001) 103 (4) 899-919.
Journal code: 7605074. ISSN: 0306-4522.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200106
ENTRY DATE: Entered STN: 20010702
Last Updated on STN: 20010702
Entered Medline: 20010628

L2 ANSWER 28 OF 73 MEDLINE DUPLICATE 14
ACCESSION NUMBER: 2001231252 MEDLINE
DOCUMENT NUMBER: 21219399 PubMed ID: 11319556
TITLE: KCNK2: reversible conversion of a hippocampal potassium
leak into a voltage-dependent channel.
COMMENT: Comment in: Nat Neurosci. 2001 May;4(5):457-8
AUTHOR: Bockenhauer D; Zilberberg N; Goldstein S A
CORPORATE SOURCE: Departments of Pediatrics and Cellular and Molecular
Physiology, Boyer Center for Molecular Medicine, Yale University School of Medicine, New Haven, Connecticut 06536, USA.
SOURCE: NATURE NEUROSCIENCE, (2001 May) 4 (5) 486-91.
Journal code: 9809671. ISSN: 1097-6256.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200105
ENTRY DATE: Entered STN: 20010529
Last Updated on STN: 20010529
Entered Medline: 20010524

L2 ANSWER 29 OF 73 SCISEARCH COPYRIGHT 2002 ISI (R) DUPLICATE 15
ACCESSION NUMBER: 2001:382496 SCISEARCH
THE GENUINE ARTICLE: 427NN
TITLE: Beam me up, Scottie! ***TREK*** channels swing both
ways
AUTHOR: Maylie J; Adelman J P (Reprint)
CORPORATE SOURCE: Oregon Hlth Sci Univ, Vollum Inst, 3181 SW Sam Jackson Pk
Rd, Portland, OR 97201 USA (Reprint); Oregon Hlth Sci Univ, Vollum Inst, Portland, OR 97201 USA; Oregon Hlth Sci
Univ, Dept Obstet & Gynecol, Portland, OR 97201 USA
COUNTRY OF AUTHOR: USA
SOURCE: NATURE NEUROSCIENCE, (MAY 2001) Vol. 4, No. 5, pp. 457-458
Publisher: NATURE AMERICA INC, 345 PARK AVE SOUTH, NEW
YORK, NY 10010-1707 USA.
ISSN: 1097-6256.
DOCUMENT TYPE: News Announcement; Journal
LANGUAGE: English
REFERENCE COUNT: 14
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L2 ANSWER 30 OF 73 MEDLINE DUPLICATE 16
ACCESSION NUMBER: 2001403113 MEDLINE
DOCUMENT NUMBER: 21347345 PubMed ID: 11454447
TITLE: Lipid and mechano-gated 2P domain K(+) channels.
AUTHOR: Patel A J; Lazdunski M; Honore E
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire,
CNRS-UMR 6097, 660 route des Lucioles, Sophia Antipolis, 06560, Valbonne, France.
SOURCE: CURRENT OPINION IN CELL BIOLOGY, (2001 Aug) 13 (4) 422-8.
Ref: 44
Journal code: 8913428. ISSN: 0955-0674.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW LITERATURE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010827
Last Updated on STN: 20010827
Entered Medline: 20010823

L2 ANSWER 31 OF 73 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:566568 BIOSIS
DOCUMENT NUMBER: PREV200100566568
TITLE: Leak ***potassium*** ***channels*** with two pore
domains.
AUTHOR(S): Lesage, F. (1); Reyes, R. (1); Lazdunski, M. (1); Barhanin,
J. (1)
CORPORATE SOURCE: (1) Institut de Pharmacologie Moleculaire et Cellulaire -
CNRS - UMR 6097, 660 Route des Lucioles, Sophia Antipolis,
06560, Valbonne France
SOURCE: Kidney & Blood Pressure Research, (2001) Vol. 24, No. 4-6,
pp. 402-405. print.
Meeting Info.: Joint Scientific Meeting of the Nephrology Society and the German Working Group for Clinical Nephrology Munster, Germany September 29-October 02, 2001
ISSN: 1420-4096.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L2 ANSWER 32 OF 73 MEDLINE DUPLICATE 17
ACCESSION NUMBER: 2001264970 MEDLINE
DOCUMENT NUMBER: 21256344 PubMed ID: 11356506
TITLE: Properties and modulation of mammalian 2P domain K+ channels.
AUTHOR: Patel A J; Honore E
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire,
CNRS-UMR6097, 660 route des Lucioles, Sophia Antipolis, 06560, Valbonne, France.
SOURCE: TRENDS IN NEUROSCIENCES, (2001 Jun) 24 (6) 339-46. Ref: 65
Journal code: 7808616. ISSN: 0166-2236.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW LITERATURE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010806
Last Updated on STN: 20010806
Entered Medline: 20010802

L2 ANSWER 33 OF 73 MEDLINE DUPLICATE 18
ACCESSION NUMBER: 2001464485 MEDLINE
DOCUMENT NUMBER: 21400471 PubMed ID: 11509450
TITLE: A ***TREK*** -1-like ***potassium*** ***channel***
in atrial cells inhibited by beta-adrenergic stimulation and activated by volatile anesthetics.
AUTHOR: Terrenoire C; Lauritzen I; Lesage F; Romey G; Lazdunski M
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire, Sophia
Antipolis, Valbonne, France.
SOURCE: CIRCULATION RESEARCH, (2001 Aug 17) 89 (4) 336-42.
Journal code: 0047103. ISSN: 1524-4571.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010820
Last Updated on STN: 20010903
Entered Medline: 20010830

L2 ANSWER 34 OF 73 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 19
ACCESSION NUMBER: 2001:473895 BIOSIS
DOCUMENT NUMBER: PREV200100473895
TITLE: The electrophysiological characteristics of the mechanosensitive two-pore domain ***potassium*** ***channel*** in dorsal root ganglion.
AUTHOR(S): Lim, In Ja (1); Kim, Kyoung Tae (1); Bang, Hyoweon (1)
CORPORATE SOURCE: (1) Department of Physiology, Chung-Ang University, College
of Medicine, Chung-Ang: heeyun@cau.ac.kr South Korea
SOURCE: Chung-Ang Journal of Medicine, (June, 2001) Vol. 26, No. 2,
pp. 105-115. print.
ISSN: 0253-6250.
DOCUMENT TYPE: Article
LANGUAGE: Korean
SUMMARY LANGUAGE: English

L2 ANSWER 35 OF 73 MEDLINE
ACCESSION NUMBER: 2001543584 MEDLINE
DOCUMENT NUMBER: 21473899 PubMed ID: 11589988
TITLE: A comparative study of three cranial sensory ganglia projecting into the oral cavity: in situ hybridization analyses of neurotrophin receptors and thermosensitive cation channels.
AUTHOR: Matsumoto I; Emori Y; Ninomiya Y; Abe K
CORPORATE SOURCE: Department of Applied Biological Chemistry, Graduate School
of Agricultural and Life Sciences, The University of Tokyo, 1-1-1 Yayoi, Bunkyo-ku, 113-8657, Tokyo, Japan.
SOURCE: BRAIN RESEARCH. MOLECULAR BRAIN RESEARCH, (2001 Sep 30) 93
(2) 105-12.
Journal code: 8908640. ISSN: 0169-328X.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200201
ENTRY DATE: Entered STN: 20011010
Last Updated on STN: 20020125
Entered Medline: 20020107

L2 ANSWER 36 OF 73 MEDLINE DUPLICATE 20
ACCESSION NUMBER: 2001245400 MEDLINE
DOCUMENT NUMBER: 21105923 PubMed ID: 11165377
TITLE: Distribution analysis of human two pore domain ***potassium*** ***channels*** in tissues of the central nervous system and periphery.
AUTHOR: Medhurst A D; Rennie G; Chapman C G; Meadows H; Duckworth M
D; Kelsell R E; Gloger I I; Pangalos M N
CORPORATE SOURCE: Neuroscience Research, SmithKline Beecham Pharmaceuticals,
New Frontiers Science Park, Essex CM19 5AW, Harlow, UK.
SOURCE: BRAIN RESEARCH. MOLECULAR BRAIN RESEARCH, (2001 Jan 31) 86
(1-2) 101-14.
Journal code: 8908640. ISSN: 0169-328X.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200105
ENTRY DATE: Entered STN: 20010517
Last Updated on STN: 20010517
Entered Medline: 20010510

L2 ANSWER 37 OF 73 MEDLINE DUPLICATE 21
ACCESSION NUMBER: 2001234321 MEDLINE
DOCUMENT NUMBER: 21095653 PubMed ID: 11172753
TITLE: The neuroprotective agent sipatrigine (BW619C89) potently
inhibits the human tandem pore-domain K(+) channels ***TREK*** -1 and TRAAK.
AUTHOR: Meadows H J; Chapman C G; Duckworth D M; Kelsell R E;
Murdock P R; Nasir S; Rennie G; Randall A D
CORPORATE SOURCE: Neuroscience Research, SmithKline Beecham Pharmaceuticals,
New Frontiers Science Park, Third Avenue, Harlow, Essex CM19 5AW, UK.. helen_j_meadows@sbphrd.com
SOURCE: BRAIN RESEARCH, (2001 Feb 16) 892 (1) 94-101.
Journal code: 0045503. ISSN: 0006-8993.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200105
ENTRY DATE: Entered STN: 20010517
Last Updated on STN: 20010517
Entered Medline: 20010503

L2 ANSWER 38 OF 73 MEDLINE DUPLICATE 22
ACCESSION NUMBER: 2001291138 MEDLINE
DOCUMENT NUMBER: 21268449 PubMed ID: 11374070
TITLE: Synergistic interaction and the role of C-terminus in the activation of TRAAK K+ channels by pressure, free fatty acids and alkali.
AUTHOR: Kim Y; Bang H; Gnatenco C; Kim D
CORPORATE SOURCE: Department of Physiology and Biophysics, Finch University
of Health Sciences, Chicago Medical School, 3333 Green Bay Road, North Chicago, IL 60064, USA.
SOURCE: PFLUGERS ARCHIV. EUROPEAN JOURNAL OF PHYSIOLOGY, (2001 Apr)
442 (1) 64-72.
Journal code: 0154720. ISSN: 0031-6768.
PUB. COUNTRY: Germany: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF302842
ENTRY MONTH: 200111
ENTRY DATE: Entered STN: 20011105
Last Updated on STN: 20011105
Entered Medline: 20011101

L2 ANSWER 39 OF 73 WPIDS (C) 2002 THOMSON DERWENT DUPLICATE 23
ACCESSION NUMBER: 2000-549146 [50] WPIDS
DOC. NO. NON-CPI: N2000-406246
DOC. NO. CPI: C2000-163964
TITLE: Novel nucleic acid encoding a ***TREK*** -1 ***potassium*** ***channel*** protein for transfecting cells to be used to identify compounds with anesthetic properties.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): HONORE, E; LAZDUNSKI, M; LESAGE, F; PATEL, A J; ROMEY, G
PATENT ASSIGNEE(S): (CNRS) CNRS CENT NAT RECH SCI; (CNRS) CENT NAT RECH SCI
COUNTRY COUNT: 90
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 2000047738	A2	20000817	(200050)*	EN	26

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL
OA PT SD SE SL SZ TZ UG ZW
W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM EE ES
FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS
LT LU LV MA MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL
TJ TM TR TT TZ UA UG UZ VN YU ZA ZW
AU 2000026854 A 20000829 (200062)
EP 1144624 A2 20011017 (200169) EN
R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE
JP 2002536017 W 20021029 (200274) 45

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 2000047738	A2	WO 2000-IB226	20000211
AU 2000026854	A	AU 2000-26854	20000211
EP 1144624	A2	EP 2000-905230	20000211
		WO 2000-IB226	20000211
JP 2002536017	W	JP 2000-598636	20000211
		WO 2000-IB226	20000211

FILING DETAILS:

PATENT NO	KIND	PATENT NO
AU 2000026854	A Based on	WO 200047738
EP 1144624	A2 Based on	WO 200047738
JP 2002536017	W Based on	WO 200047738

PRIORITY APPLN. INFO: US 2000-503089 20000211; US 1999-119727P 19990212

L2 ANSWER 40 OF 73 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:861503 CAPLUS
DOCUMENT NUMBER: 134:25373
TITLE: ***Potassium*** ***channel*** -related h-TREK1 polypeptides and polynucleotides for treatment of nervous system disorders
INVENTOR(S): Hervieu, Guillaume Jean; Meadows, Helen Jane; Randall, Andrew David
PATENT ASSIGNEE(S): Smithkline Beecham PLC, UK
SOURCE: PCT Int. Appl., 35 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000072863	A2	20001207	WO 2000-GB2107	20000601
WO 2000072863	A3	20010222		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
EP 1187627 A2 20020320 EP 2000-935374 20000601
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO
PRIORITY APPLN. INFO.: GB 1999-12733 A 19990601
WO 2000-GB2107 W 20000601

L2 ANSWER 41 OF 73 MEDLINE DUPLICATE 24
ACCESSION NUMBER: 2001105970 MEDLINE
DOCUMENT NUMBER: 20564271 PubMed ID: 10993907
TITLE: Simultaneous activation of p38 MAPK and p42/44 MAPK by ATP stimulates the K+ current ITREK in cardiomyocytes.
AUTHOR: Aimond F; Rauzier J M; Bony C; Vassort G
CORPORATE SOURCE: INSERM U-390, Physiopathologie cardiovasculaire, IFR N degrees 3, CHU Arnaud de Villeneuve, F-34295 Montpellier Cedex 5, France.
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2000 Dec 15) 275 (50) 39110-6.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200102
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010208

L2 ANSWER 42 OF 73 MEDLINE
ACCESSION NUMBER: 2000496079 MEDLINE
DOCUMENT NUMBER: 20435789 PubMed ID: 10880510
TITLE: Human TREK2, a 2P domain mechano-sensitive K+ channel with multiple regulations by polyunsaturated fatty acids, lysophospholipids, and Gs, Gi, and Gq protein-coupled receptors.
AUTHOR: Lesage F; Terrenoire C; Romey G; Lazdunski M
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire, CNRS-UPR 411, 660 route des Lucioles, Sophia Antipolis, 06560 Valbonne, France.
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2000 Sep 15) 275 (37) 28398-405.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF279890
ENTRY MONTH: 200010
ENTRY DATE: Entered STN: 20001027
Last Updated on STN: 20001027
Entered Medline: 20001013

L2 ANSWER 43 OF 73 MEDLINE DUPLICATE 25
ACCESSION NUMBER: 2000298807 MEDLINE
DOCUMENT NUMBER: 20298807 PubMed ID: 10747911
TITLE: ***TREK*** -2, a new member of the mechanosensitive tandem-pore K+ channel family.
AUTHOR: Bang H; Kim Y; Kim D
CORPORATE SOURCE: Department of Physiology and Biophysics, Finch University of Health Sciences/The Chicago Medical School, North Chicago, Illinois 60064, USA.
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2000 Jun 9) 275 (23) 17412-9.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Space Life Sciences
OTHER SOURCE: GENBANK-AF196965
ENTRY MONTH: 200007
ENTRY DATE: Entered STN: 20000728
Last Updated on STN: 20000728
Entered Medline: 20000720

L2 ANSWER 44 OF 73 MEDLINE DUPLICATE 26
ACCESSION NUMBER: 2000209381 MEDLINE
DOCUMENT NUMBER: 20209381 PubMed ID: 10744694
TITLE: Lysophospholipids open the two-pore domain mechano-gated K(+) channels ***TREK*** -1 and TRAAK.
AUTHOR: Maingret F; Patel A J; Lesage F; Lazdunski M; Honore E
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire, CNRS UPR 411, Sophia Antipolis, 06560 Valbonne, France.
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2000 Apr 7) 275 (14) 10128-33.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200005
ENTRY DATE: Entered STN: 20000518
Last Updated on STN: 20000518
Entered Medline: 20000508

L2 ANSWER 45 OF 73 MEDLINE DUPLICATE 27
ACCESSION NUMBER: 2000200422 MEDLINE
DOCUMENT NUMBER: 20200422 PubMed ID: 10734076
TITLE: TASK-3, a new member of the tandem pore K(+) channel family.
AUTHOR: Kim Y; Bang H; Kim D
CORPORATE SOURCE: Department of Physiology and Biophysics, Finch University of Health Sciences/The Chicago Medical School, North Chicago, Illinois 60064, USA.
CONTRACT NUMBER: HL55363 (NHLBI)
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2000 Mar 31) 275 (13) 9340-7.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF192366
ENTRY MONTH: 200005
ENTRY DATE: Entered STN: 20000512
Last Updated on STN: 20000512
Entered Medline: 20000504

L2 ANSWER 46 OF 73 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 2000:779832 SCISEARCH
THE GENUINE ARTICLE: 361ZC
TITLE: Mutants of a temperature-sensitive two-P domain ***potassium*** ***channel***
AUTHOR: Kunkel M T; Johnstone D B; Thomas J H; Salkoff L (Reprint)
CORPORATE SOURCE: WASHINGTON UNIV, SCH MED, DEPT ANAT & NEUROBIOL, 660 S EUCLID AVE, BOX 8108, ST LOUIS, MO 63110 (Reprint); WASHINGTON UNIV, SCH MED, DEPT ANAT & NEUROBIOL, ST LOUIS, MO 63110; WASHINGTON UNIV, SCH MED, DEPT GENET, ST LOUIS, MO 63110; UNIV WASHINGTON, DEPT GENET, SEATTLE, WA 98195
COUNTRY OF AUTHOR: USA
SOURCE: JOURNAL OF NEUROSCIENCE, (15 OCT 2000) Vol. 20, No. 20, pp. 7517-7524.
Publisher: SOC NEUROSCIENCE, 11 DUPONT CIRCLE, NW, STE 500, WASHINGTON, DC 20036.
ISSN: 0270-6474.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: English
REFERENCE COUNT: 37
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L2 ANSWER 47 OF 73 MEDLINE DUPLICATE 28
ACCESSION NUMBER: 2000296674 MEDLINE
DOCUMENT NUMBER: 20296674 PubMed ID: 10835347
TITLE: ***TREK*** -1 is a heat-activated background K(+) channel.
AUTHOR: Maingret F; Lauritzen I; Patel A J; Heurteaux C; Reyes R; Lesage F; Lazdunski M; Honore E
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire, CNRS UPR 411, 660 route des Lucioles, Sophia Antipolis, 06560 Valbonne, France.. ipmc@ipmc.cnrs.fr
SOURCE: EMBO JOURNAL, (2000 Jun 1) 19 (11) 2483-91.
Journal code: 8208664. ISSN: 0261-4189.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200007
ENTRY DATE: Entered STN: 20000728
Last Updated on STN: 20000728
Entered Medline: 20000720

L2 ANSWER 48 OF 73 MEDLINE DUPLICATE 29
ACCESSION NUMBER: 2000237615 MEDLINE
DOCUMENT NUMBER: 20237615 PubMed ID: 10775263
TITLE: Polyunsaturated fatty acids are potent neuroprotectors.
AUTHOR: Lauritzen I; Blondeau N; Heurteaux C; Widmann C; Romey G; Lazdunski M
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire, CNRS UPR 411, 660 route des Lucioles, Sophia Antipolis, 06560 Valbonne, France.
SOURCE: EMBO JOURNAL, (2000 Apr 17) 19 (8) 1784-93.
Journal code: 8208664. ISSN: 0261-4189.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200006
ENTRY DATE: Entered STN: 20000622
Last Updated on STN: 20000622
Entered Medline: 20000613

L2 ANSWER 49 OF 73 MEDLINE DUPLICATE 30
ACCESSION NUMBER: 2000251453 MEDLINE
DOCUMENT NUMBER: 20251453 PubMed ID: 10790857
TITLE: Axonal transport of ***TREK*** and TRAAK ***potassium*** ***channels*** in rat sciatic nerves.
AUTHOR: Bearzatto B; Lesage F; Reyes R; Lazdunski M; Laduron P M
CORPORATE SOURCE: Laboratory of Neurophysiology, Universite Libre de Bruxelles, Belgium.
SOURCE: NEUROREPORT, (2000 Apr 7) 11 (5) 927-30.
Journal code: 9100935. ISSN: 0959-4965.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200007
ENTRY DATE: Entered STN: 20000720
Last Updated on STN: 20000720
Entered Medline: 20000710

L2 ANSWER 50 OF 73 MEDLINE DUPLICATE 31

ACCESSION NUMBER: 2000242005 MEDLINE
DOCUMENT NUMBER: 20242005 PubMed ID: 10779373
TITLE: The neuroprotective agent riluzole activates the two P domain K(+) channels ***TREK*** -1 and TRAAK.
AUTHOR: Duprat F; Lesage F; Patel A J; Fink M; Romey G; Lazdunski M
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire, Centre
National de la Recherche Scientifique, Valbonne, France.
SOURCE: MOLECULAR PHARMACOLOGY, (2000 May) 57 (5) 906-12.
Journal code: 0035623. ISSN: 0026-895X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200005
ENTRY DATE: Entered STN: 20000606
Last Updated on STN: 20000606
Entered Medline: 20000525

L2 ANSWER 51 OF 73 MEDLINE DUPLICATE 32
ACCESSION NUMBER: 2001040741 MEDLINE
DOCUMENT NUMBER: 20508366 PubMed ID: 11053038
TITLE: Molecular and functional properties of two-pore-domain ***potassium*** ***channels*** .
AUTHOR: Lesage F; Lazdunski M
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire, et Cellulaire,
Centre National de la Recherche Scientifique-Unite Propre de Recherche 411, Sophia Antipolis, 06560 Valbonne, France.
SOURCE: AMERICAN JOURNAL OF PHYSIOLOGY. RENAL PHYSIOLOGY, (2000
Nov) 279 (5) F793-801. Ref: 64
Journal code: 100901990. ISSN: 0363-6127.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200012
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001207

L2 ANSWER 52 OF 73 MEDLINE DUPLICATE 33
ACCESSION NUMBER: 2000244931 MEDLINE
DOCUMENT NUMBER: 20244931 PubMed ID: 10784345
TITLE: Cloning, localisation and functional expression of the human orthologue of the ***TREK*** -1 ***potassium*** ***channel*** .
AUTHOR: Meadows H J; Benham C D; Cairns W; Gloger I; Jennings C;
Medhurst A D; Murdock P; Chapman C G
CORPORATE SOURCE: Neuroscience Research, SmithKline Beecham Pharmaceuticals,
Harlow, Essex, UK.. Helen_J_Meadows@sbphrd.com
SOURCE: PFLUGERS ARCHIV. EUROPEAN JOURNAL OF PHYSIOLOGY, (2000 Apr)
439 (6) 714-22.
Journal code: 0154720. ISSN: 0031-6768.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF171068
ENTRY MONTH: 200006
ENTRY DATE: Entered STN: 20000629
Last Updated on STN: 20000629
Entered Medline: 20000621

L2 ANSWER 53 OF 73 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2000:178435 BIOSIS
DOCUMENT NUMBER: PREV200000178435
TITLE: ***TREK*** -2, a new member of the mammalian mechanosensitive K+ channel family.
AUTHOR(S): Bang, Hyoweon (1); Kim, Yangmi (1); Kim, Donghee (1)
CORPORATE SOURCE: (1) Chicago Medical School, 3333 Green Bay Road, North
Chicago, IL, 60064 USA
SOURCE: Biophysical Journal, (Jan., 2000) Vol. 78, No. 1 Part 2, pp. 474A.
Meeting Info.: 44th Annual Meeting of the Biophysical Society. New Orleans, Louisiana, USA February 12-16, 2000
ISSN: 0006-3495.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L2 ANSWER 54 OF 73 MEDLINE DUPLICATE 34
ACCESSION NUMBER: 2000488784 MEDLINE
DOCUMENT NUMBER: 20492877 PubMed ID: 11039733
TITLE: Localization of the tandem pore domain K+ channel TASK-1 in
the rat central nervous system.
AUTHOR: Kindler C H; Pietruck C; Yost C S; Sampson E R; Gray A T
CORPORATE SOURCE: Department of Anesthesia, University of Basel, Kantonsspital, Switzerland.. ckindler@uhbs.ch
CONTRACT NUMBER: GMS-51372 (NIGMS)
SOURCE: BRAIN RESEARCH. MOLECULAR BRAIN RESEARCH, (2000 Aug 14) 80
(1) 99-108.
Journal code: 8908640. ISSN: 0169-328X.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200103
ENTRY DATE: Entered STN: 20010404
Last Updated on STN: 20010404
Entered Medline: 20010301

L2 ANSWER 55 OF 73 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE
35
ACCESSION NUMBER: 2000:353891 BIOSIS
DOCUMENT NUMBER: PREV200000353891
TITLE: Expression of ***TREK*** -1 ***potassium*** ***channel*** in GABA-containing neurons in the adult rat
CNS.
AUTHOR(S): Cluderay, J. E. (1); Meadows, H. J. (1); Hervieu, G. (1)
CORPORATE SOURCE: (1) Neuroscience Research, SB, Harlow, Essex UK
SOURCE: European Journal of Neuroscience, (2000) Vol. 12, No. Supplement 11, pp. 23. print.
Meeting Info.: Meeting of the Federation of European Neuroscience Societies Brighton, UK June 24-28, 2000
ISSN: 0953-816X.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L2 ANSWER 56 OF 73 WPIDS (C) 2002 THOMSON DERWENT DUPLICATE 36
ACCESSION NUMBER: 1999-469126 [39] WPIDS
DOC. NO. NON-CPI: N1999-350285
DOC. NO. CPI: C1999-137655
TITLE: New two pore ***potassium*** ***channel*** used
for, e.g. treatment of cancer, pulmonary, cardiovascular and inflammatory diseases.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): CHAPMAN, C G; MEADOWS, H J
PATENT ASSIGNEE(S): (SMIK) SMITHKLINE BEECHAM PLC; (CHAP-I) CHAPMAN C G;
(MEAD-I) MEADOWS H J
COUNTRY COUNT: 21
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9937762	A1	19990729	(199939)*	EN	26
RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE					
W: JP					
EP 1051485	A1	20001115	(200059)	EN	
R: BE CH DE DK FR GB IT LI NL					
US 6242217	B1	20010605	(200133)		
US 2002028485	A1	20020307	(200221)		
JP 2002511233	W	20020416	(200242)		52

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9937762	A1	WO 1998-EP7805	19981202
EP 1051485	A1	EP 1998-962402	19981202
		WO 1998-EP7805	19981202
US 6242217	B1	US 1999-236080	19990125
US 2002028485	A1 Div ex	US 1999-236080	19990125
		US 2001-828746	20010409
JP 2002511233	W	WO 1998-EP7805	19981202
		JP 2000-528670	19981202

FILING DETAILS:

PATENT NO	KIND	PATENT NO
EP 1051485	A1 Based on	WO 9937762
US 2002028485	A1 Div ex	US 6242217
JP 2002511233	W Based on	WO 9937762

PRIORITY APPLN. INFO: GB 1998-22135 19981009; EP 1998-300570
19980127

L2 ANSWER 57 OF 73 WPIDS (C) 2002 THOMSON DERWENT
ACCESSION NUMBER: 1999-551038 [46] WPIDS
DOC. NO. NON-CPI: N1999-407763
DOC. NO. CPI: C1999-160733
TITLE: New mechanically sensitive ***potassium*** ***channel*** , used to screen for specific modulators, potential therapeutic agents for heart and nervous system disorders.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): DUPRAT, F; FINK, M; HONORE, E; LAZDUNSKI, M; LESAGE, F
PATENT ASSIGNEE(S): (CNRS) CNRS CENT NAT RECH SCI
COUNTRY COUNT: 21
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9945108	A2	19990910	(199946)*	FR	40
RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE					
W: CA JP US					
FR 2775688	A1	19990910	(199946)		
EP 1058726	A2	20001213	(200066)	FR	
R: DE ES FR GB IT					
JP 2002505102	W	20020219	(200216)		41

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9945108	A2	WO 1999-FR404	19990223
FR 2775688	A1	FR 1998-2725	19980305
EP 1058726	A2	EP 1999-904937	19990223
		WO 1999-FR404	19990223
JP 2002505102	W	WO 1999-FR404	19990223
		JP 2000-534640	19990223

FILING DETAILS:

PATENT NO	KIND	PATENT NO
EP 1058726	A2 Based on	WO 9945108
JP 2002505102	W Based on	WO 9945108

PRIORITY APPLN. INFO: FR 1998-2725 19980305

L2 ANSWER 58 OF 73 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1999:566066 CAPLUS
DOCUMENT NUMBER: 131:168355
TITLE: Identification of human genes for K+Hnov ***potassium*** ***channels*** by gene discovery methods and their investigative, diagnostic, and therapeutic uses
INVENTOR(S): Miller, Andrew P.; Curran, Mark Edward; Hu, Ping;
Rutter, Marc; Wang, Jian-ying
PATENT ASSIGNEE(S): Axys Pharmaceuticals, Inc., USA
SOURCE: PCT Int. Appl., 112 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9943696	A1	19990902	WO 1999-US3826	19990222
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2321194	AA	19990902	CA 1999-2321194	19990222
AU 9927809	A1	19990915	AU 1999-27809	19990222
AU 747846	B2	20020523		
EP 1056765	A1	20001206	EP 1999-908356	19990222
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
US 6399761	B1	20020604	US 1999-336643	19990618
PRIORITY APPLN. INFO.:			US 1998-76687P	P 19980225
			US 1998-95836P	P 19980807
			US 1999-116448P	P 19990119
			WO 1999-US3826	W 19990222

REFERENCE COUNT: 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 59 OF 73 MEDLINE DUPLICATE 37
ACCESSION NUMBER: 1999410397 MEDLINE
DOCUMENT NUMBER: 99410397 PubMed ID: 10480871
TITLE: Mechano- or acid stimulation, two interactive modes of activation of the ***TREK*** -1 ***potassium*** ***channel*** .
AUTHOR: Maingret F; Patel A J; Lesage F; Lazdunski M; Honore E
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire, CNRS
UPR 411, 660 route des Lucioles, Sophia Antipolis, 06560 Valbonne, France.
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1999 Sep 17) 274 (38)
26691-6.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Space Life Sciences

ENTRY MONTH: 199910
ENTRY DATE: Entered STN: 19991026
Last Updated on STN: 19991026
Entered Medline: 19991013

L2 ANSWER 60 OF 73 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2000:137222 BIOSIS
DOCUMENT NUMBER: PREV200000137222
TITLE: Cloning, localisation and functional expression of a novel human 2P domain ***potassium*** ***channel*** .
AUTHOR(S): Meadows, H. J. (1); Chapman, C. G.; Jennings, C. (1); Hervieu, G. (1); Cluderay, J. (1); Randall, A. R. (1); Gloger, I. S.; Benham, C. D. (1)
CORPORATE SOURCE: (1) Neuroscience, SmithKline Beecham Pharmaceuticals, Third
Avenue, New Frontiers Science Park North, Harlow, Essex, CM19 5AW UK
SOURCE: Society for Neuroscience Abstracts., (1999) Vol. 25, No.
1-2, pp. 2248.
Meeting Info.: 29th Annual Meeting of the Society for Neuroscience. Miami Beach, Florida, USA October 23-28, 1999
Society for Neuroscience
. ISSN: 0190-5295.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L2 ANSWER 61 OF 73 MEDLINE DUPLICATE 38
ACCESSION NUMBER: 1999098876 MEDLINE
DOCUMENT NUMBER: 99098876 PubMed ID: 9880510
TITLE: TRAAK is a mammalian neuronal mechano-gated K+ channel.
AUTHOR: Maingret F; Fosset M; Lesage F; Lazdunski M; Honore E
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire,
CNRS-UPR 411, 660 route des Lucioles, Sophia Antipolis, 06560 Valbonne, France.
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1999 Jan 15) 274 (3)
1381-7.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Space Life Sciences
ENTRY MONTH: 199902
ENTRY DATE: Entered STN: 19990223
Last Updated on STN: 19990223
Entered Medline: 19990211

L2 ANSWER 62 OF 73 MEDLINE DUPLICATE 39
ACCESSION NUMBER: 1999215865 MEDLINE
DOCUMENT NUMBER: 99215865 PubMed ID: 10201682
TITLE: Local anesthetic inhibition of baseline ***potassium*** ***channels*** with two pore domains in tandem.
AUTHOR: Kindler C H; Yost C S; Gray A T
CORPORATE SOURCE: Department of Anesthesia, University of California, San
Francisco 94143-0542, USA.
CONTRACT NUMBER: GMS-51372 (NIGMS)
SOURCE: ANESTHESIOLOGY, (1999 Apr) 90 (4) 1092-102.
Journal code: 1300217. ISSN: 0003-3022.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
ENTRY MONTH: 199904
ENTRY DATE: Entered STN: 19990504
Last Updated on STN: 19990504
Entered Medline: 19990421

L2 ANSWER 63 OF 73 MEDLINE DUPLICATE 40
ACCESSION NUMBER: 1999254548 MEDLINE
DOCUMENT NUMBER: 99254548 PubMed ID: 10321245
TITLE: Inhalational anesthetics activate two-pore-domain background K+ channels.
AUTHOR: Patel A J; Honore E; Lesage F; Fink M; Romey G; Lazdunski M
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire-CNRS-UPR 411, Valbonne, France.
SOURCE: NATURE NEUROSCIENCE, (1999 May) 2 (5) 422-6.
Journal code: 9809671. ISSN: 1097-6256.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199905
ENTRY DATE: Entered STN: 19990607
Last Updated on STN: 19990607
Entered Medline: 19990525

L2 ANSWER 64 OF 73 MEDLINE DUPLICATE 41
ACCESSION NUMBER: 1999103971 MEDLINE
DOCUMENT NUMBER: 99103971 PubMed ID: 9887061
TITLE: Potential identification of the O2-sensitive K+ current in a human neuroepithelial body-derived cell line.
AUTHOR: O'Kelly I; Stephens R H; Peers C; Kemp P J
CORPORATE SOURCE: School of Biomedical Sciences, University of Leeds, Leeds
LS2 9JT, United Kingdom.
SOURCE: AMERICAN JOURNAL OF PHYSIOLOGY, (1999 Jan) 276 (1 Pt 1)
L96-L104.
Journal code: 0370511. ISSN: 0002-9513.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199903
ENTRY DATE: Entered STN: 19990324
Last Updated on STN: 19990324
Entered Medline: 19990309

L2 ANSWER 65 OF 73 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 1999:85877 SCISEARCH
THE GENUINE ARTICLE: 158ED
TITLE: Potential identification of the O-2-sensitive K+ current in a human neuroepithelial body-derived cell line
AUTHOR: OKelly I; Stephens R H; Peers C; Kemp P J (Reprint)
CORPORATE SOURCE: UNIV LEEDS, SCH BIOMED SCI, WORSLEY MED & DENT BLDG, LEEDS
LS2 9JT, W YORKSHIRE, ENGLAND (Reprint); UNIV LEEDS, SCH
BIOMED SCI, LEEDS LS2 9JT, W YORKSHIRE, ENGLAND; UNIV
LEEDS, INST CARDIOVASC RES, LEEDS LS2 9JT, W YORKSHIRE,
ENGLAND
COUNTRY OF AUTHOR: ENGLAND
SOURCE: AMERICAN JOURNAL OF PHYSIOLOGY-LUNG CELLULAR AND MOLECULAR
PHYSIOLOGY, (JAN 1999) Vol. 20, No. 1, pp. L96-L104.
Publisher: AMER PHYSIOLOGICAL SOC, 9650 ROCKVILLE PIKE,
BETHESDA, MD 20814.
ISSN: 1040-0605.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: English
REFERENCE COUNT: 25
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L2 ANSWER 66 OF 73 MEDLINE DUPLICATE 42
ACCESSION NUMBER: 1999030343 MEDLINE
DOCUMENT NUMBER: 99030343 PubMed ID: 9812978
TITLE: Cloning and expression of a novel pH-sensitive two pore domain K+ channel from human kidney.
AUTHOR: Reyes R; Duprat F; Lesage F; Fink M; Salinas M; Farman N;
Lazdunski M
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire,
CNRS-UPR 411, 660 route des Lucioles, Sophia Antipolis, 06560 Valbonne, France.
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1998 Nov 20) 273 (47)
30863-9.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF084830
ENTRY MONTH: 199812
ENTRY DATE: Entered STN: 19990115
Last Updated on STN: 19990115
Entered Medline: 19981221

L2 ANSWER 67 OF 73 MEDLINE DUPLICATE 43
ACCESSION NUMBER: 1998353454 MEDLINE
DOCUMENT NUMBER: 98353454 PubMed ID: 9687497
TITLE: A mammalian two pore domain mechano-gated S-like K+ channel.
AUTHOR: Patel A J; Honore E; Maingret F; Lesage F; Fink M; Duprat
F; Lazdunski M
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire, CNRS,
Valbonne, France.
SOURCE: EMBO JOURNAL, (1998 Aug 3) 17 (15) 4283-90.
Journal code: 8208664. ISSN: 0261-4189.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199809
ENTRY DATE: Entered STN: 19981006
Last Updated on STN: 19981006
Entered Medline: 19980922

L2 ANSWER 68 OF 73 MEDLINE DUPLICATE 44
ACCESSION NUMBER: 1998292450 MEDLINE
DOCUMENT NUMBER: 98292450 PubMed ID: 9628867
TITLE: A neuronal two P domain K+ channel stimulated by arachidonic acid and polyunsaturated fatty acids.
AUTHOR: Fink M; Lesage F; Duprat F; Heurteaux C; Reyes R; Fosset M;
Lazdunski M
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire-CNRS-UPR 411, Valbonne, France.
SOURCE: EMBO JOURNAL, (1998 Jun 15) 17 (12) 3297-308.
Journal code: 8208664. ISSN: 0261-4189.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF056492
ENTRY MONTH: 199807
ENTRY DATE: Entered STN: 19980811
Last Updated on STN: 20000303
Entered Medline: 19980730

L2 ANSWER 69 OF 73 MEDLINE DUPLICATE 45
ACCESSION NUMBER: 1998099797 MEDLINE
DOCUMENT NUMBER: 98099797 PubMed ID: 9437008
TITLE: An open rectifier ***potassium*** ***channel*** with two pore domains in tandem cloned from rat cerebellum.
AUTHOR: Leonoudakis D; Gray A T; Winegar B D; Kindler C H; Harada
M; Taylor D M; Chavez R A; Forsayeth J R; Yost C S
CORPORATE SOURCE: Department of Anesthesia, University of California San
Francisco, San Francisco, California 94143-0542, USA.
CONTRACT NUMBER: GM-08440 (NIGMS)
GMS-51372 (NIGMS)
SOURCE: JOURNAL OF NEUROSCIENCE, (1998 Feb 1) 18 (3) 868-77.
Journal code: 8102140. ISSN: 0270-6474.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF031384
ENTRY MONTH: 199802
ENTRY DATE: Entered STN: 19980224
Last Updated on STN: 20000303
Entered Medline: 19980206

L2 ANSWER 70 OF 73 MEDLINE DUPLICATE 46
ACCESSION NUMBER: 1998165556 MEDLINE
DOCUMENT NUMBER: 98165556 PubMed ID: 9506712
TITLE: Cloning and functional expression of a novel cardiac two-pore background K+ channel (cTBAK-1).
AUTHOR: Kim D; Fujita A; Horio Y; Kurachi Y
CORPORATE SOURCE: Department of Pharmacology II, Faculty of Medicine, Osaka
University, Suita, Japan.
SOURCE: CIRCULATION RESEARCH, (1998 Mar 9) 82 (4) 513-8.
Journal code: 0047103. ISSN: 0009-7330.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB008537
ENTRY MONTH: 199803
ENTRY DATE: Entered STN: 19980410
Last Updated on STN: 19980410
Entered Medline: 19980327

L2 ANSWER 71 OF 73 MEDLINE DUPLICATE 47
ACCESSION NUMBER: 1998389638 MEDLINE
DOCUMENT NUMBER: 98389638 PubMed ID: 9721223
TITLE: Mapping of human ***potassium*** ***channel*** genes ***TREK*** -1 (KCNK2) and TASK (KCNK3) to chromosomes 1q41 and 2p23.
AUTHOR: Lesage F; Lazdunski M
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire, CNRS,
Valbonne, 660 route des Lucioles, Sophia Antipolis, 06560, France.
SOURCE: GENOMICS, (1998 Aug 1) 51 (3) 478-9.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF006823
ENTRY MONTH: 199810
ENTRY DATE: Entered STN: 19981020
Last Updated on STN: 19981020
Entered Medline: 19981005

L2 ANSWER 72 OF 73 MEDLINE DUPLICATE 48
ACCESSION NUMBER: 97459932 MEDLINE
DOCUMENT NUMBER: 97459932 PubMed ID: 9312005
TITLE: TASK, a human background K+ channel to sense external pH
variations near physiological pH.
AUTHOR: Duprat F; Lesage F; Fink M; Reyes R; Heurteaux C; Lazdunski
M
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire, CNRS,
660 route des Lucioles, Sophia Antipolis, 06560 Valbonne, France.
SOURCE: EMBO JOURNAL, (1997 Sep 1) 16 (17) 5464-71.
Journal code: 8208664. ISSN: 0261-4189.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF006823; GENBANK-AF006824
ENTRY MONTH: 199712
ENTRY DATE: Entered STN: 19980109
Last Updated on STN: 19980109

Entered Medline: 19971215

L2 ANSWER 73 OF 73 MEDLINE DUPLICATE 49
ACCESSION NUMBER: 97157476 MEDLINE
DOCUMENT NUMBER: 97157476 PubMed ID: 9003761
TITLE: Cloning, functional expression and brain localization of a novel unconventional outward rectifier K+ channel.
AUTHOR: Fink M; Duprat F; Lesage F; Reyes R; Romey G; Heurteaux C; Lazdunski M
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire, CNRS, Valbonne, France.
SOURCE: EMBO JOURNAL, (1996 Dec 16) 15 (24) 6854-62. Journal code: 8208664. ISSN: 0261-4189.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U73488
ENTRY MONTH: 199702
ENTRY DATE: Entered STN: 19970227
Last Updated on STN: 19980206
Entered Medline: 19970213

FILE 'MEDLINE' ENTERED
FILE 'JAPIO' ENTERED
FILE 'BIOSIS'
FILE 'SCISEARCH'
FILE 'WPIDS'
FILE 'CAPLUS'
FILE 'EMBASE'
=> potassium channel and trek
L1 217 POTASSIUM CHANNEL AND TREK

=> dup rem l1
PROCESSING COMPLETED FOR L1
L2 73 DUP REM L1 (144 DUPLICATES REMOVED)

=> d ibib l2 1-73

L2 ANSWER 1 OF 73 MEDLINE
ACCESSION NUMBER: 2002165854 MEDLINE
DOCUMENT NUMBER: 21896085 PubMed ID: 11897836
TITLE: The ***TREK*** two P domain K+ channels.
COMMENT: Comment on: J Physiol. 2002 Mar 15;539(Pt 3):657-68
AUTHOR: Patel Amanda; Honore Eric
CORPORATE SOURCE: IPMC-CNRS, 660 Route des Lucioles, Sophia Antipolis, 06560
Valbonne, France.
SOURCE: JOURNAL OF PHYSIOLOGY, (2002 Mar 15) 539 (Pt 3) 647.
Journal code: 0266262. ISSN: 0022-3751.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Commentary
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200206
ENTRY DATE: Entered STN: 20020319
Last Updated on STN: 20020621
Entered Medline: 20020620

L2 ANSWER 2 OF 73 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 2002266838 MEDLINE
DOCUMENT NUMBER: 22001365 PubMed ID: 11886861
TITLE: Modulation of TASK-1 (Kcnk3) and TASK-3 (Kcnk9) ***potassium*** ***channels*** : volatile anesthetics and neurotransmitters share a molecular site of action.
AUTHOR: Talley Edmund M; Bayliss Douglas A
CORPORATE SOURCE: Department of Pharmacology, University of Virginia,
Charlottesville, Virginia 22908-0735, USA..
emt3m@virginia.edu
CONTRACT NUMBER: NS33583 (NINDS)
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2002 May 17) 277 (20)
17733-42.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF031384; GENBANK-AF391084
ENTRY MONTH: 200207
ENTRY DATE: Entered STN: 20020514
Last Updated on STN: 20020717
Entered Medline: 20020716

L2 ANSWER 3 OF 73 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 2002322564 MEDLINE
DOCUMENT NUMBER: 22060496 PubMed ID: 12065410
TITLE: An intracellular proton sensor commands lipid- and mechano-gating of the K(+) channel ***TREK*** -1.
AUTHOR: Honore Eric; Maingret Francois; Lazdunski Michel; Patel
Amanda Jane
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire,
CNRS-UMR 6097, 660 route des Lucioles, Sophia Antipolis, F-06560 Valbonne, France.
SOURCE: EMBO JOURNAL, (2002 Jun 17) 21 (12) 2968-76.
Journal code: 8208664. ISSN: 0261-4189.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200208
ENTRY DATE: Entered STN: 20020615
Last Updated on STN: 20020830
Entered Medline: 20020829

L2 ANSWER 4 OF 73 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 2002238785 MEDLINE
DOCUMENT NUMBER: 21972941 PubMed ID: 11976378
TITLE: Long-term alteration of S-type potassium current and passive membrane properties in aplysia sensory neurons following axotomy.
AUTHOR: Ungless Mark A; Gasull Xavier; Walters Edgar T
CORPORATE SOURCE: Department of Integrative Biology and Pharmacology,
University of Texas-Houston Medical School, Houston, Texas
77030, USA.
CONTRACT NUMBER: NS-35882 (NINDS)
NS-35979 (NINDS)
RR-10294 (NCRR)
SOURCE: JOURNAL OF NEUROPHYSIOLOGY, (2002 May) 87 (5) 2408-20.
Journal code: 0375404. ISSN: 0022-3077.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Space Life Sciences
ENTRY MONTH: 200206
ENTRY DATE: Entered STN: 20020429
Last Updated on STN: 20020824
Entered Medline: 20020628

L2 ANSWER 5 OF 73 MEDLINE DUPLICATE 4
ACCESSION NUMBER: 2002191200 MEDLINE
DOCUMENT NUMBER: 21896087 PubMed ID: 11897838
TITLE: Expression pattern and functional characteristics of two novel splice variants of the two-pore-domain ***potassium*** ***channel*** ***TREK*** -2.
COMMENT: Comment in: J Physiol. 2002 Mar 15;539(Pt 3):647
AUTHOR: Gu Wenli; Schlichthorl Gunter; Hirsch Jochen R; Engels
Hartmut; Karschin Christine; Karschin Andreas; Derst Christian; Steinlein Ortrud K; Daut Jurgen
CORPORATE SOURCE: Institut fur Humangenetik, Universitat Bonn, Wilhelmstrasse
31, D-53111 Bonn, Germany.
SOURCE: JOURNAL OF PHYSIOLOGY, (2002 Mar 15) 539 (Pt 3) 657-68.
Journal code: 0266262. ISSN: 0022-3751.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200206
ENTRY DATE: Entered STN: 20020403
Last Updated on STN: 20020621
Entered Medline: 20020620

L2 ANSWER 6 OF 73 CAPLUS COPYRIGHT 2002 ACS DUPLICATE 5
ACCESSION NUMBER: 2002:322996 CAPLUS
DOCUMENT NUMBER: 137:43030
TITLE: The ***TREK*** two P domain K+ channels
AUTHOR(S): Patel, Amanda; Honore, Eric
CORPORATE SOURCE: IPMC-CNRS, Valbonne, 06560, Fr.
SOURCE: Journal of Physiology (Cambridge, United Kingdom) (2002), 539(3), 647
CODEN: JPHYA7; ISSN: 0022-3751
PUBLISHER: Cambridge University Press
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
REFERENCE COUNT: 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 7 OF 73 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:365502 BIOSIS
DOCUMENT NUMBER: PREV200200365502
TITLE: Several tandem-pore K+ channels contribute to background K+
current in cerebellar granule neurons.
AUTHOR(S): Han, Jaehee (1); Truell, Jeffrey (1); Gnatenco, Carmen (1);
Kim, Donghee (1)
CORPORATE SOURCE: (1) Chicago Medical School, Chicago USA
SOURCE: Biophysical Journal, (January, 2002) Vol. 82, No. 1 Part 2,
pp. 636a. http://intl.biophysj.org/. print.
Meeting Info.: 46th Annual Meeting of the Biophysical Society San Francisco, California, USA February 23-27, 2002
ISSN: 0006-3495.
DOCUMENT TYPE: Conference
LANGUAGE: English

L2 ANSWER 8 OF 73 MEDLINE DUPLICATE 6
ACCESSION NUMBER: 2002376647 IN-PROCESS
DOCUMENT NUMBER: 22117977 PubMed ID: 12122143
TITLE: Characterization of four types of background ***potassium*** ***channels*** in rat cerebellar granule neurons.
AUTHOR: Han Jaehee; Truell Jeffrey; Gnatenco Carmen; Kim Donghee
CORPORATE SOURCE: Department of Physiology, Gyeongsang National University
School of Medicine, Chinju, Korea.
SOURCE: JOURNAL OF PHYSIOLOGY, (2002 Jul 15) 542 (Pt 2) 431-44.
Journal code: 0266262. ISSN: 0022-3751.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020718
Last Updated on STN: 20020718

L2 ANSWER 9 OF 73 MEDLINE
ACCESSION NUMBER: 2002309957 MEDLINE
DOCUMENT NUMBER: 22047240 PubMed ID: 12051718
TITLE: Validation of a quantitative method for real time PCR kinetics.
AUTHOR: Liu Weihong; Saint David A
CORPORATE SOURCE: Department of Physiology, University of Adelaide, Adelaide,
SA 5005, Australia.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2002
Jun 7) 294 (2) 347-53.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
(VALIDATION STUDIES)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200207
ENTRY DATE: Entered STN: 20020611
Last Updated on STN: 20020717
Entered Medline: 20020716

L2 ANSWER 10 OF 73 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:363310 BIOSIS
DOCUMENT NUMBER: PREV200200363310
TITLE: Expression pattern and functional characteristics of two novel splice variants of the two-pore-domain ***potassium*** ***channel*** ***TREK*** -2.
AUTHOR(S): Gu, W. (1); Schlichthoerl, G. (1); Hirsch, J. R. (1); Engels, H. (1); Karschin, C. (1); Karschin, A. (1); Derst, C. (1); Daut, J. (1)
CORPORATE SOURCE: (1) Institut fuer Normale und Pathologische Physiologie,
Universitaet Marburg, Deutschhausstrasse 2, 35037, Marburg Germany
SOURCE: Pfluegers Archiv European Journal of Physiology, (March,
2002) Vol. 443, No. Supplement 1, pp. S341.
http://link.springer.de/link/service/journals/00424/.
print.
Meeting Info.: 81st Annual Joint Meeting of the Physiological Society, the Scandinavian Physiological Society and the German Physiological Society Tuebingen, Germany March 15-19, 2002
ISSN: 0031-6768.
DOCUMENT TYPE: Conference
LANGUAGE: English

L2 ANSWER 11 OF 73 MEDLINE DUPLICATE 7
ACCESSION NUMBER: 2002174336 MEDLINE
DOCUMENT NUMBER: 21903759 PubMed ID: 11906167
TITLE: Molecular basis of the voltage-dependent gating of ***TREK*** -1, a mechano-sensitive K(+) channel.
AUTHOR: Maingret Francois; Honore Eric; Lazdunski Michel; Patel
Amanda Jane
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire, CNRS,
UMR 6097, Sophia Antipolis, Valbonne, France.
SOURCE: BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2002
Mar 29) 292 (2) 339-46.
Journal code: 0372516. ISSN: 0006-291X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200205
ENTRY DATE: Entered STN: 20020322
Last Updated on STN: 20020507
Entered Medline: 20020506

L2 ANSWER 12 OF 73 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
ACCESSION NUMBER: 2002372279 EMBASE
TITLE: Background ***potassium*** ***channels*** move into
focus.
AUTHOR: Mathie A.; Clarke C.E.
CORPORATE SOURCE: A. Mathie, Biophysics Section, Blackett Laboratory,
Department of Biological Sciences, Prince Consort Road, London SW7 2BW, United Kingdom. a.mathie@ic.ac.uk
SOURCE: Journal of Physiology, (15 Jul 2002) 542/2 (334).
Refs: 7
ISSN: 0022-3751 CODEN: JPHYA7
COUNTRY: United Kingdom
DOCUMENT TYPE: Journal; Article
FILE SEGMENT: 002 Physiology
008 Neurology and Neurosurgery
LANGUAGE: English

L2 ANSWER 13 OF 73 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:387362 BIOSIS
DOCUMENT NUMBER: PREV200200387362
TITLE: Identification of twin-pore ***potassium*** ***channels*** in rat mesenteric arteries.
AUTHOR(S): Gardener, M. J. (1); Burnham, M. P. (1); Gilling, K. E.
(1); Johnson, I. T. (1); Edwards, G. (1); Weston, A. H. (1)
CORPORATE SOURCE: (1) School of Biological Sciences, University of
Manchester, Oxford Road, G.38 Stopford Building, Manchester, M13 9PT UK
SOURCE: British Journal of Pharmacology, (March, 2002) Vol. 135,
No. Proceedings Supplement, pp. 307P.
http://www.brjpharmacol.org/. print.

Meeting Info.: Meeting of the British Pharmacological Society London, England, UK December 17-21, 2001
ISSN: 0007-1188.
DOCUMENT TYPE: Conference
LANGUAGE: English

L2 ANSWER 14 OF 73 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:387339 BIOSIS
DOCUMENT NUMBER: PREV200200387339
TITLE: Twin-pore domain ***potassium*** ***channels*** in
rat pulmonary artery: Potential candidates of hypoxic pulmonary vasoconstriction.
AUTHOR(S): Johnson, I. T. (1); Gardener, M. J. (1); Richards, G. (1);
Burnham, M. (1); Glen, C. D. (1); Edwards, G. (1); Weston, A. H. (1)
CORPORATE SOURCE: (1) School of Biological Sciences, University of
Manchester, Oxford Road, G38 Stopford Building, Manchester,
M13 9PT UK
SOURCE: British Journal of Pharmacology, (March, 2002) Vol. 135,
No. Proceedings Supplement, pp. 284P.
http://www.brjpharmacol.org/. print.
Meeting Info.: Meeting of the British Pharmacological Society London, England, UK December 17-21, 2001
ISSN: 0007-1188.
DOCUMENT TYPE: Conference
LANGUAGE: English

L2 ANSWER 15 OF 73 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2002:322118 BIOSIS
DOCUMENT NUMBER: PREV200200322118
TITLE: Functional expression of ***TREK*** -2 K+ channel in cultured rat brain astrocytes.
AUTHOR(S): Gnatenco, Carmen (1); Kim, Donghee
CORPORATE SOURCE: (1) Chicago Medical School, 3333 Green Bay Road, North
Chicago, IL, 60064 USA
SOURCE: Biophysical Journal, (January, 2002) Vol. 82, No. 1 Part 2,
pp. 270a. http://intl.biophysj.org/. print.
Meeting Info.: 46th Annual Meeting of the Biophysical Society San Francisco, California, USA February 23-27, 2002
ISSN: 0006-3495.
DOCUMENT TYPE: Conference
LANGUAGE: English

L2 ANSWER 16 OF 73 MEDLINE DUPLICATE 8
ACCESSION NUMBER: 2002159167 MEDLINE
DOCUMENT NUMBER: 21888939 PubMed ID: 11891578
TITLE: ***Trek*** -like ***potassium*** ***channels***
in rat cardiac ventricular myocytes are activated by intracellular ATP.
AUTHOR: Tan J H C; Liu W; Saint D A
CORPORATE SOURCE: Cellular Biophysics Laboratory, The Department of
Physiology, University of Adelaide, Adelaide SA 5005, Australia.
SOURCE: JOURNAL OF MEMBRANE BIOLOGY, (2002 Feb 1) 185 (3) 201-7.
Journal code: 0211301. ISSN: 0022-2631.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200207
ENTRY DATE: Entered STN: 20020314
Last Updated on STN: 20020713
Entered Medline: 20020712

L2 ANSWER 17 OF 73 MEDLINE DUPLICATE 9
ACCESSION NUMBER: 2002165318 MEDLINE
DOCUMENT NUMBER: 21895240 PubMed ID: 11897089
TITLE: Functional expression of ***TREK*** -2 K+ channel in cultured rat brain astrocytes.
AUTHOR: Gnatenco Carmen; Han Jaehee; Snyder Ann K; Kim Donghee
CORPORATE SOURCE: Department of Physiology and Biophysics, Finch University
of Health Sciences/The Chicago Medical School, 3333 Green Bay Road, North Chicago, IL 60064-3095, USA.
SOURCE: BRAIN RESEARCH, (2002 Mar 22) 931 (1) 56-67.
Journal code: 0045503. ISSN: 0006-8993.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200205
ENTRY DATE: Entered STN: 20020319
Last Updated on STN: 20020522
Entered Medline: 20020520

L2 ANSWER 18 OF 73 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2002:113616 CAPLUS
DOCUMENT NUMBER: 137:104322
TITLE: A New Quantitative Method of Real Time Reverse Transcription Polymerase Chain Reaction Assay Based on Simulation of Polymerase Chain Reaction Kinetics
AUTHOR(S): Liu, Weihong; Saint, David A.
CORPORATE SOURCE: Department of Physiology, University of Adelaide,
Adelaide, 5005, Australia
SOURCE: Analytical Biochemistry (2002), 302(1), 52-59
CODEN: ANBCA2; ISSN: 0003-2697
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 19 OF 73 MEDLINE
ACCESSION NUMBER: 2001231249 MEDLINE
DOCUMENT NUMBER: 21219392 PubMed ID: 11319549
TITLE: Beam me up, Scottie! ***TREK*** channels swing both
ways.
COMMENT: Comment on: Nat Neurosci. 2001 May;4(5):486-91
AUTHOR: Maylie J; Adelman J P
SOURCE: NATURE NEUROSCIENCE, (2001 May) 4 (5) 457-8.
Journal code: 9809671. ISSN: 1097-6256.
PUB. COUNTRY: United States
DOCUMENT TYPE: Commentary
News Announcement
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200105
ENTRY DATE: Entered STN: 20010529
Last Updated on STN: 20010529
Entered Medline: 20010524

L2 ANSWER 20 OF 73 MEDLINE DUPLICATE 10
ACCESSION NUMBER: 2001667665 MEDLINE
DOCUMENT NUMBER: 21570223 PubMed ID: 11560940
TITLE: ***TREK*** -1 regulation by nitric oxide and cGMP-dependent protein kinase. An essential role in smooth muscle inhibitory neurotransmission.
AUTHOR: Koh S D; Monaghan K; Sergeant G P; Ro S; Walker R L;
Sanders K M; Horowitz B
CORPORATE SOURCE: Department of Physiology and Cell Biology, University of
Nevada School of Medicine, Reno, Nevada 89557, USA.
CONTRACT NUMBER: DK 41315 (NIDDK)
HL 49254 (NHLBI)
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2001 Nov 23) 276 (47)
44338-46.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200112
ENTRY DATE: Entered STN: 20011120
Last Updated on STN: 20020123
Entered Medline: 20011220

L2 ANSWER 21 OF 73 MEDLINE DUPLICATE 11
ACCESSION NUMBER: 2001520013 MEDLINE
DOCUMENT NUMBER: 21450949 PubMed ID: 11567039
TITLE: Cns distribution of members of the two-pore-domain (KCNK)
potassium ***channel*** family.
AUTHOR: Talley E M; Solorzano G; Lei Q; Kim D; Bayliss D A
CORPORATE SOURCE: Department of Pharmacology, University of Virginia,
Charlottesville, Virginia 22908, USA.. emt3m@virginia.edu
CONTRACT NUMBER: MH12091 (NIMH)
NS33583 (NINDS)
SOURCE: JOURNAL OF NEUROSCIENCE, (2001 Oct 1) 21 (19) 7491-505.
Journal code: 8102140. ISSN: 1529-2401.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200110
ENTRY DATE: Entered STN: 20010924
Last Updated on STN: 20011015
Entered Medline: 20011011

L2 ANSWER 22 OF 73 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 2001:240967 SCISEARCH
THE GENUINE ARTICLE: 410MC
TITLE: THIK-1 and THIK-2, a novel subfamily of tandem pore domain
K+ channels
AUTHOR: Rajan S; Wischmeyer E; Karschin C; Preisig-Muller R; Grzeschik K H; Daut J; Karschin A (Reprint); Derst C
CORPORATE SOURCE: Univ Marburg, Inst Humangenet, D-35032 Marburg, Germany
(Reprint); Univ Marburg, Inst Normal & Pathol Physiol, D-35032 Marburg, Germany; Max Planck Inst Biophys Chem,
D-37070 Gottingen, Germany
COUNTRY OF AUTHOR: Germany
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (9 MAR 2001) Vol. 276,
No. 10, pp. 7302-7311.
Publisher: AMER SOC BIOCHEMISTRY MOLECULAR BIOLOGY INC,
9650 ROCKVILLE PIKE, BETHESDA, MD 20814 USA.
ISSN: 0021-9258.
DOCUMENT TYPE: Article; Journal
LANGUAGE: English
REFERENCE COUNT: 32
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L2 ANSWER 23 OF 73 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:562734 BIOSIS
DOCUMENT NUMBER: PREV200100562734
TITLE: SB-209712, a submicromolar inhibitor of ***TREK*** -1
potassium ***channels*** .
AUTHOR(S): Meadows, H. J. (1); Ray, A. M. (1); Heath, J. (1); Gager,
T. (1); Leslie, R. A. (1); Randall, A. D. (1)
CORPORATE SOURCE: (1) Neuroscience Research, GlaxoSmithKline, Harlow UK
SOURCE: Society for Neuroscience Abstracts, (2001) Vol. 27, No. 2,
pp. 1864. print.
Meeting Info.: 31st Annual Meeting of the Society for Neuroscience San Diego, California, USA November 10-15, 2001
ISSN: 0190-5295.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L2 ANSWER 24 OF 73 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:562721 BIOSIS
DOCUMENT NUMBER: PREV200100562721
TITLE: CNS distribution of members of the two-pore-domain (KCNK)
potassium ***channel*** family.
AUTHOR(S): Talley, E. M. (1); Solorzano, G. (1); Lei, Q. (1); Kim, D.;
Bayliss, D. A. (1)
CORPORATE SOURCE: (1) Dept. Pharmacol., Univ. of Virginia, Charlottesville,
VA USA
SOURCE: Society for Neuroscience Abstracts, (2001) Vol. 27, No. 2,
pp. 1862. print.
Meeting Info.: 31st Annual Meeting of the Society for Neuroscience San Diego, California, USA November 10-15, 2001
ISSN: 0190-5295.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L2 ANSWER 25 OF 73 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 2001:797985 SCISEARCH
THE GENUINE ARTICLE: 479JU
TITLE: Anesthetic-sensitive 2P domain K+ channels
AUTHOR: Patel A J; Honore E (Reprint)
CORPORATE SOURCE: Inst Pharmacol Mol & Cellulaire, CNRS UMR6097, 600 Route
Lucioles, F-06560 Valbonne, France (Reprint); Inst Pharmacol Mol & Cellulaire, CNRS UMR6097, F-06560 Valbonne, France
COUNTRY OF AUTHOR: France
SOURCE: ANESTHESIOLOGY, (OCT 2001) Vol. 95, No. 4, pp. 1013-1021.
Publisher: LIPPINCOTT WILLIAMS & WILKINS, 530 WALNUT ST,
PHILADELPHIA, PA 19106-3621 USA.
ISSN: 0003-3022.
DOCUMENT TYPE: General Review; Journal
LANGUAGE: English
REFERENCE COUNT: 67

L2 ANSWER 26 OF 73 MEDLINE DUPLICATE 12
ACCESSION NUMBER: 2001572938 MEDLINE
DOCUMENT NUMBER: 21535328 PubMed ID: 11680629
TITLE: Localization of ***TREK*** -2 K+ channel domains that
regulate channel kinetics and sensitivity to pressure, fatty acids and pHi.
AUTHOR: Kim Y; Gnatenco C; Bang H; Kim D
CORPORATE SOURCE: Department of Physiology and Biophysics, Finch University
of Health Sciences, The Chicago Medical School, IL 60064, USA.. donghee.kim@finchcms.edu
SOURCE: PFLUGERS ARCHIV. EUROPEAN JOURNAL OF PHYSIOLOGY, (2001 Sep)
442 (6) 952-60.
Journal code: 0154720. ISSN: 0031-6768.
PUB. COUNTRY: Germany: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200202
ENTRY DATE: Entered STN: 20011030
Last Updated on STN: 20020222
Entered Medline: 20020221

L2 ANSWER 27 OF 73 MEDLINE DUPLICATE 13

ACCESSION NUMBER: 2001370005 MEDLINE
DOCUMENT NUMBER: 21198116 PubMed ID: 11301200
TITLE: Distribution and expression of ***TREK*** -1, a two-pore-domain ***potassium*** ***channel*** , in the adult rat CNS.
AUTHOR: Hervieu G J; Cluderay J E; Gray C W; Green P J; Ranson J L;
Randall A D; Meadows H J
CORPORATE SOURCE: Neuroscience Research, SmithKline Beecham Pharmaceuticals,
Third Avenue, Essex CM19 5AW, Harlow, UK.
SOURCE: NEUROSCIENCE, (2001) 103 (4) 899-919.
Journal code: 7605074. ISSN: 0306-4522.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200106
ENTRY DATE: Entered STN: 20010702
Last Updated on STN: 20010702
Entered Medline: 20010628

L2 ANSWER 28 OF 73 MEDLINE DUPLICATE 14
ACCESSION NUMBER: 2001231252 MEDLINE
DOCUMENT NUMBER: 21219399 PubMed ID: 11319556
TITLE: KCNK2: reversible conversion of a hippocampal potassium
leak into a voltage-dependent channel.
COMMENT: Comment in: Nat Neurosci. 2001 May;4(5):457-8
AUTHOR: Bockenhauer D; Zilberberg N; Goldstein S A
CORPORATE SOURCE: Departments of Pediatrics and Cellular and Molecular
Physiology, Boyer Center for Molecular Medicine, Yale University School of Medicine, New Haven, Connecticut 06536, USA.
SOURCE: NATURE NEUROSCIENCE, (2001 May) 4 (5) 486-91.
Journal code: 9809671. ISSN: 1097-6256.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200105
ENTRY DATE: Entered STN: 20010529
Last Updated on STN: 20010529
Entered Medline: 20010524

L2 ANSWER 29 OF 73 SCISEARCH COPYRIGHT 2002 ISI (R) DUPLICATE 15
ACCESSION NUMBER: 2001:382496 SCISEARCH
THE GENUINE ARTICLE: 427NN
TITLE: Beam me up, Scottie! ***TREK*** channels swing both
ways
AUTHOR: Maylie J; Adelman J P (Reprint)
CORPORATE SOURCE: Oregon Hlth Sci Univ, Vollum Inst, 3181 SW Sam Jackson Pk
Rd, Portland, OR 97201 USA (Reprint); Oregon Hlth Sci Univ, Vollum Inst, Portland, OR 97201 USA; Oregon Hlth Sci
Univ, Dept Obstet & Gynecol, Portland, OR 97201 USA
COUNTRY OF AUTHOR: USA
SOURCE: NATURE NEUROSCIENCE, (MAY 2001) Vol. 4, No. 5, pp. 457-458
Publisher: NATURE AMERICA INC, 345 PARK AVE SOUTH, NEW
YORK, NY 10010-1707 USA.
ISSN: 1097-6256.
DOCUMENT TYPE: News Announcement; Journal
LANGUAGE: English
REFERENCE COUNT: 14
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L2 ANSWER 30 OF 73 MEDLINE DUPLICATE 16
ACCESSION NUMBER: 2001403113 MEDLINE
DOCUMENT NUMBER: 21347345 PubMed ID: 11454447
TITLE: Lipid and mechano-gated 2P domain K(+) channels.
AUTHOR: Patel A J; Lazdunski M; Honore E
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire,
CNRS-UMR 6097, 660 route des Lucioles, Sophia Antipolis, 06560, Valbonne, France.
SOURCE: CURRENT OPINION IN CELL BIOLOGY, (2001 Aug) 13 (4) 422-8.
Ref: 44
Journal code: 8913428. ISSN: 0955-0674.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW LITERATURE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010827
Last Updated on STN: 20010827
Entered Medline: 20010823

L2 ANSWER 31 OF 73 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:566568 BIOSIS
DOCUMENT NUMBER: PREV200100566568
TITLE: Leak ***potassium*** ***channels*** with two pore
domains.
AUTHOR(S): Lesage, F. (1); Reyes, R. (1); Lazdunski, M. (1); Barhanin,
J. (1)
CORPORATE SOURCE: (1) Institut de Pharmacologie Moleculaire et Cellulaire -
CNRS - UMR 6097, 660 Route des Lucioles, Sophia Antipolis,
06560, Valbonne France
SOURCE: Kidney & Blood Pressure Research, (2001) Vol. 24, No. 4-6,
pp. 402-405. print.
Meeting Info.: Joint Scientific Meeting of the Nephrology Society and the German Working Group for Clinical Nephrology Munster, Germany September 29-October 02, 2001
ISSN: 1420-4096.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L2 ANSWER 32 OF 73 MEDLINE DUPLICATE 17
ACCESSION NUMBER: 2001264970 MEDLINE
DOCUMENT NUMBER: 21256344 PubMed ID: 11356506
TITLE: Properties and modulation of mammalian 2P domain K+ channels.
AUTHOR: Patel A J; Honore E
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire,
CNRS-UMR6097, 660 route des Lucioles, Sophia Antipolis, 06560, Valbonne, France.
SOURCE: TRENDS IN NEUROSCIENCES, (2001 Jun) 24 (6) 339-46. Ref: 65
Journal code: 7808616. ISSN: 0166-2236.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW LITERATURE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010806
Last Updated on STN: 20010806
Entered Medline: 20010802

L2 ANSWER 33 OF 73 MEDLINE DUPLICATE 18
ACCESSION NUMBER: 2001464485 MEDLINE
DOCUMENT NUMBER: 21400471 PubMed ID: 11509450
TITLE: A ***TREK*** -1-like ***potassium*** ***channel***
in atrial cells inhibited by beta-adrenergic stimulation and activated by volatile anesthetics.
AUTHOR: Terrenoire C; Lauritzen I; Lesage F; Romey G; Lazdunski M
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire, Sophia
Antipolis, Valbonne, France.
SOURCE: CIRCULATION RESEARCH, (2001 Aug 17) 89 (4) 336-42.
Journal code: 0047103. ISSN: 1524-4571.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010820
Last Updated on STN: 20010903
Entered Medline: 20010830

L2 ANSWER 34 OF 73 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE 19
ACCESSION NUMBER: 2001:473895 BIOSIS
DOCUMENT NUMBER: PREV200100473895
TITLE: The electrophysiological characteristics of the mechanosensitive two-pore domain ***potassium*** ***channel*** in dorsal root ganglion.
AUTHOR(S): Lim, In Ja (1); Kim, Kyoung Tae (1); Bang, Hyoweon (1)
CORPORATE SOURCE: (1) Department of Physiology, Chung-Ang University, College
of Medicine, Chung-Ang: heeyun@cau.ac.kr South Korea
SOURCE: Chung-Ang Journal of Medicine, (June, 2001) Vol. 26, No. 2,
pp. 105-115. print.
ISSN: 0253-6250.
DOCUMENT TYPE: Article
LANGUAGE: Korean
SUMMARY LANGUAGE: English

L2 ANSWER 35 OF 73 MEDLINE
ACCESSION NUMBER: 2001543584 MEDLINE
DOCUMENT NUMBER: 21473899 PubMed ID: 11589988
TITLE: A comparative study of three cranial sensory ganglia projecting into the oral cavity: in situ hybridization analyses of neurotrophin receptors and thermosensitive cation channels.
AUTHOR: Matsumoto I; Emori Y; Ninomiya Y; Abe K
CORPORATE SOURCE: Department of Applied Biological Chemistry, Graduate School
of Agricultural and Life Sciences, The University of Tokyo, 1-1-1 Yayoi, Bunkyo-ku, 113-8657, Tokyo, Japan.
SOURCE: BRAIN RESEARCH. MOLECULAR BRAIN RESEARCH, (2001 Sep 30) 93
(2) 105-12.
Journal code: 8908640. ISSN: 0169-328X.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200201
ENTRY DATE: Entered STN: 20011010
Last Updated on STN: 20020125
Entered Medline: 20020107

L2 ANSWER 36 OF 73 MEDLINE DUPLICATE 20
ACCESSION NUMBER: 2001245400 MEDLINE
DOCUMENT NUMBER: 21105923 PubMed ID: 11165377
TITLE: Distribution analysis of human two pore domain ***potassium*** ***channels*** in tissues of the central nervous system and periphery.
AUTHOR: Medhurst A D; Rennie G; Chapman C G; Meadows H; Duckworth M
D; Kelsell R E; Gloger I I; Pangalos M N
CORPORATE SOURCE: Neuroscience Research, SmithKline Beecham Pharmaceuticals,
New Frontiers Science Park, Essex CM19 5AW, Harlow, UK.
SOURCE: BRAIN RESEARCH. MOLECULAR BRAIN RESEARCH, (2001 Jan 31) 86
(1-2) 101-14.
Journal code: 8908640. ISSN: 0169-328X.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200105
ENTRY DATE: Entered STN: 20010517
Last Updated on STN: 20010517
Entered Medline: 20010510

L2 ANSWER 37 OF 73 MEDLINE DUPLICATE 21
ACCESSION NUMBER: 2001234321 MEDLINE
DOCUMENT NUMBER: 21095653 PubMed ID: 11172753
TITLE: The neuroprotective agent sipatrigine (BW619C89) potently
inhibits the human tandem pore-domain K(+) channels ***TREK*** -1 and TRAAK.
AUTHOR: Meadows H J; Chapman C G; Duckworth D M; Kelsell R E;
Murdock P R; Nasir S; Rennie G; Randall A D
CORPORATE SOURCE: Neuroscience Research, SmithKline Beecham Pharmaceuticals,
New Frontiers Science Park, Third Avenue, Harlow, Essex CM19 5AW, UK.. helen_j_meadows@sbphrd.com
SOURCE: BRAIN RESEARCH, (2001 Feb 16) 892 (1) 94-101.
Journal code: 0045503. ISSN: 0006-8993.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200105
ENTRY DATE: Entered STN: 20010517
Last Updated on STN: 20010517
Entered Medline: 20010503

L2 ANSWER 38 OF 73 MEDLINE DUPLICATE 22
ACCESSION NUMBER: 2001291138 MEDLINE
DOCUMENT NUMBER: 21268449 PubMed ID: 11374070
TITLE: Synergistic interaction and the role of C-terminus in the activation of TRAAK K+ channels by pressure, free fatty acids and alkali.
AUTHOR: Kim Y; Bang H; Gnatenco C; Kim D
CORPORATE SOURCE: Department of Physiology and Biophysics, Finch University
of Health Sciences, Chicago Medical School, 3333 Green Bay Road, North Chicago, IL 60064, USA.
SOURCE: PFLUGERS ARCHIV. EUROPEAN JOURNAL OF PHYSIOLOGY, (2001 Apr)
442 (1) 64-72.
Journal code: 0154720. ISSN: 0031-6768.
PUB. COUNTRY: Germany: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF302842
ENTRY MONTH: 200111
ENTRY DATE: Entered STN: 20011105
Last Updated on STN: 20011105
Entered Medline: 20011101

L2 ANSWER 39 OF 73 WPIDS (C) 2002 THOMSON DERWENT DUPLICATE 23
ACCESSION NUMBER: 2000-549146 [50] WPIDS
DOC. NO. NON-CPI: N2000-406246
DOC. NO. CPI: C2000-163964
TITLE: Novel nucleic acid encoding a ***TREK*** -1 ***potassium*** ***channel*** protein for transfecting cells to be used to identify compounds with anesthetic properties.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): HONORE, E; LAZDUNSKI, M; LESAGE, F; PATEL, A J; ROMEY, G
PATENT ASSIGNEE(S): (CNRS) CNRS CENT NAT RECH SCI; (CNRS) CENT NAT RECH SCI
COUNTRY COUNT: 90
PATENT INFORMATION:

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PATENT NO KIND DATE WEEK LA PG

WO 2000047738 A2 20000817 (200050)* EN 26
RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL
OA PT SD SE SL SZ TZ UG ZW
W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM EE ES
FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS
LT LU LV MA MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL
TJ TM TR TT TZ UA UG UZ VN YU ZA ZW
AU 2000026854 A 20000829 (200062)
EP 1144624 A2 20011017 (200169) EN
R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE
JP 2002536017 W 20021029 (200274) 45

APPLICATION DETAILS:

PATENT NO KIND APPLICATION DATE

WO 2000047738 A2 WO 2000-IB226 20000211
AU 2000026854 A AU 2000-26854 20000211
EP 1144624 A2 EP 2000-905230 20000211
WO 2000-IB226 20000211
JP 2002536017 W JP 2000-598636 20000211
WO 2000-IB226 20000211

FILING DETAILS:

PATENT NO KIND PATENT NO

AU 2000026854 A Based on WO 200047738
EP 1144624 A2 Based on WO 200047738
JP 2002536017 W Based on WO 200047738

PRIORITY APPLN. INFO: US 2000-503089 20000211; US 1999-119727P 19990212

L2 ANSWER 40 OF 73 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2000:861503 CAPLUS
DOCUMENT NUMBER: 134:25373
TITLE: ***Potassium*** ***channel*** -related h-TREK1 polypeptides and polynucleotides for treatment of nervous system disorders
INVENTOR(S): Hervieu, Guillaume Jean; Meadows, Helen Jane; Randall, Andrew David
PATENT ASSIGNEE(S): Smithkline Beecham PLC, UK
SOURCE: PCT Int. Appl., 35 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO. KIND DATE APPLICATION NO. DATE

WO 2000072863 A2 20001207 WO 2000-GB2107 20000601
WO 2000072863 A3 20010222
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
EP 1187627 A2 20020320 EP 2000-935374 20000601
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO
PRIORITY APPLN. INFO.: GB 1999-12733 A 19990601
WO 2000-GB2107 W 20000601

L2 ANSWER 41 OF 73 MEDLINE DUPLICATE 24
ACCESSION NUMBER: 2001105970 MEDLINE
DOCUMENT NUMBER: 20564271 PubMed ID: 10993907
TITLE: Simultaneous activation of p38 MAPK and p42/44 MAPK by ATP stimulates the K+ current ITREK in cardiomyocytes.
AUTHOR: Aimond F; Rauzier J M; Bony C; Vassort G
CORPORATE SOURCE: INSERM U-390, Physiopathologie cardiovasculaire, IFR N degrees 3, CHU Arnaud de Villeneuve, F-34295 Montpellier Cedex 5, France.
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2000 Dec 15) 275 (50) 39110-6.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200102
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20010208

L2 ANSWER 42 OF 73 MEDLINE
ACCESSION NUMBER: 2000496079 MEDLINE
DOCUMENT NUMBER: 20435789 PubMed ID: 10880510
TITLE: Human TREK2, a 2P domain mechano-sensitive K+ channel with multiple regulations by polyunsaturated fatty acids, lysophospholipids, and Gs, Gi, and Gq protein-coupled receptors.
AUTHOR: Lesage F; Terrenoire C; Romey G; Lazdunski M
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire, CNRS-UPR 411, 660 route des Lucioles, Sophia Antipolis, 06560 Valbonne, France.
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2000 Sep 15) 275 (37) 28398-405.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF279890
ENTRY MONTH: 200010
ENTRY DATE: Entered STN: 20001027
Last Updated on STN: 20001027
Entered Medline: 20001013

L2 ANSWER 43 OF 73 MEDLINE DUPLICATE 25
ACCESSION NUMBER: 2000298807 MEDLINE
DOCUMENT NUMBER: 20298807 PubMed ID: 10747911
TITLE: ***TREK*** -2, a new member of the mechanosensitive tandem-pore K+ channel family.
AUTHOR: Bang H; Kim Y; Kim D
CORPORATE SOURCE: Department of Physiology and Biophysics, Finch University of Health Sciences/The Chicago Medical School, North Chicago, Illinois 60064, USA.
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2000 Jun 9) 275 (23) 17412-9.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Space Life Sciences
OTHER SOURCE: GENBANK-AF196965
ENTRY MONTH: 200007
ENTRY DATE: Entered STN: 20000728
Last Updated on STN: 20000728
Entered Medline: 20000720

L2 ANSWER 44 OF 73 MEDLINE DUPLICATE 26
ACCESSION NUMBER: 2000209381 MEDLINE
DOCUMENT NUMBER: 20209381 PubMed ID: 10744694
TITLE: Lysophospholipids open the two-pore domain mechano-gated K(+) channels ***TREK*** -1 and TRAAK.
AUTHOR: Maingret F; Patel A J; Lesage F; Lazdunski M; Honore E
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire, CNRS UPR 411, Sophia Antipolis, 06560 Valbonne, France.
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2000 Apr 7) 275 (14) 10128-33.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200005
ENTRY DATE: Entered STN: 20000518
Last Updated on STN: 20000518
Entered Medline: 20000508

L2 ANSWER 45 OF 73 MEDLINE DUPLICATE 27
ACCESSION NUMBER: 2000200422 MEDLINE
DOCUMENT NUMBER: 20200422 PubMed ID: 10734076
TITLE: TASK-3, a new member of the tandem pore K(+) channel family.
AUTHOR: Kim Y; Bang H; Kim D
CORPORATE SOURCE: Department of Physiology and Biophysics, Finch University of Health Sciences/The Chicago Medical School, North Chicago, Illinois 60064, USA.
CONTRACT NUMBER: HL55363 (NHLBI)
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (2000 Mar 31) 275 (13) 9340-7.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF192366
ENTRY MONTH: 200005
ENTRY DATE: Entered STN: 20000512
Last Updated on STN: 20000512
Entered Medline: 20000504

L2 ANSWER 46 OF 73 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 2000:779832 SCISEARCH
THE GENUINE ARTICLE: 361ZC
TITLE: Mutants of a temperature-sensitive two-P domain ***potassium*** ***channel***
AUTHOR: Kunkel M T; Johnstone D B; Thomas J H; Salkoff L (Reprint)
CORPORATE SOURCE: WASHINGTON UNIV, SCH MED, DEPT ANAT & NEUROBIOL, 660 S EUCLID AVE, BOX 8108, ST LOUIS, MO 63110 (Reprint); WASHINGTON UNIV, SCH MED, DEPT ANAT & NEUROBIOL, ST LOUIS, MO 63110; WASHINGTON UNIV, SCH MED, DEPT GENET, ST LOUIS, MO 63110; UNIV WASHINGTON, DEPT GENET, SEATTLE, WA 98195
COUNTRY OF AUTHOR: USA
SOURCE: JOURNAL OF NEUROSCIENCE, (15 OCT 2000) Vol. 20, No. 20, pp. 7517-7524.
Publisher: SOC NEUROSCIENCE, 11 DUPONT CIRCLE, NW, STE 500, WASHINGTON, DC 20036.
ISSN: 0270-6474.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: English
REFERENCE COUNT: 37
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L2 ANSWER 47 OF 73 MEDLINE DUPLICATE 28
ACCESSION NUMBER: 2000296674 MEDLINE
DOCUMENT NUMBER: 20296674 PubMed ID: 10835347
TITLE: ***TREK*** -1 is a heat-activated background K(+) channel.
AUTHOR: Maingret F; Lauritzen I; Patel A J; Heurteaux C; Reyes R; Lesage F; Lazdunski M; Honore E
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire, CNRS UPR 411, 660 route des Lucioles, Sophia Antipolis, 06560 Valbonne, France.. ipmc@ipmc.cnrs.fr
SOURCE: EMBO JOURNAL, (2000 Jun 1) 19 (11) 2483-91.
Journal code: 8208664. ISSN: 0261-4189.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200007
ENTRY DATE: Entered STN: 20000728
Last Updated on STN: 20000728
Entered Medline: 20000720

L2 ANSWER 48 OF 73 MEDLINE DUPLICATE 29
ACCESSION NUMBER: 2000237615 MEDLINE
DOCUMENT NUMBER: 20237615 PubMed ID: 10775263
TITLE: Polyunsaturated fatty acids are potent neuroprotectors.
AUTHOR: Lauritzen I; Blondeau N; Heurteaux C; Widmann C; Romey G; Lazdunski M
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire, CNRS UPR 411, 660 route des Lucioles, Sophia Antipolis, 06560 Valbonne, France.
SOURCE: EMBO JOURNAL, (2000 Apr 17) 19 (8) 1784-93.
Journal code: 8208664. ISSN: 0261-4189.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200006
ENTRY DATE: Entered STN: 20000622
Last Updated on STN: 20000622
Entered Medline: 20000613

L2 ANSWER 49 OF 73 MEDLINE DUPLICATE 30
ACCESSION NUMBER: 2000251453 MEDLINE
DOCUMENT NUMBER: 20251453 PubMed ID: 10790857
TITLE: Axonal transport of ***TREK*** and TRAAK ***potassium*** ***channels*** in rat sciatic nerves.
AUTHOR: Bearzatto B; Lesage F; Reyes R; Lazdunski M; Laduron P M
CORPORATE SOURCE: Laboratory of Neurophysiology, Universite Libre de Bruxelles, Belgium.
SOURCE: NEUROREPORT, (2000 Apr 7) 11 (5) 927-30.
Journal code: 9100935. ISSN: 0959-4965.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200007
ENTRY DATE: Entered STN: 20000720
Last Updated on STN: 20000720
Entered Medline: 20000710

L2 ANSWER 50 OF 73 MEDLINE DUPLICATE 31

ACCESSION NUMBER: 2000242005 MEDLINE
DOCUMENT NUMBER: 20242005 PubMed ID: 10779373
TITLE: The neuroprotective agent riluzole activates the two P domain K(+) channels ***TREK*** -1 and TRAAK.
AUTHOR: Duprat F; Lesage F; Patel A J; Fink M; Romey G; Lazdunski M
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire, Centre
National de la Recherche Scientifique, Valbonne, France.
SOURCE: MOLECULAR PHARMACOLOGY, (2000 May) 57 (5) 906-12.
Journal code: 0035623. ISSN: 0026-895X.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200005
ENTRY DATE: Entered STN: 20000606
Last Updated on STN: 20000606
Entered Medline: 20000525

L2 ANSWER 51 OF 73 MEDLINE DUPLICATE 32
ACCESSION NUMBER: 2001040741 MEDLINE
DOCUMENT NUMBER: 20508366 PubMed ID: 11053038
TITLE: Molecular and functional properties of two-pore-domain ***potassium*** ***channels*** .
AUTHOR: Lesage F; Lazdunski M
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire, et Cellulaire,
Centre National de la Recherche Scientifique-Unite Propre de Recherche 411, Sophia Antipolis, 06560 Valbonne, France.
SOURCE: AMERICAN JOURNAL OF PHYSIOLOGY. RENAL PHYSIOLOGY, (2000
Nov) 279 (5) F793-801. Ref: 64
Journal code: 100901990. ISSN: 0363-6127.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200012
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001207

L2 ANSWER 52 OF 73 MEDLINE DUPLICATE 33
ACCESSION NUMBER: 2000244931 MEDLINE
DOCUMENT NUMBER: 20244931 PubMed ID: 10784345
TITLE: Cloning, localisation and functional expression of the human orthologue of the ***TREK*** -1 ***potassium***
channel .
AUTHOR: Meadows H J; Benham C D; Cairns W; Gloger I; Jennings C;
Medhurst A D; Murdock P; Chapman C G
CORPORATE SOURCE: Neuroscience Research, SmithKline Beecham Pharmaceuticals,
Harlow, Essex, UK.. Helen_J_Meadows@sbphrd.com
SOURCE: PFLUGERS ARCHIV. EUROPEAN JOURNAL OF PHYSIOLOGY, (2000 Apr)
439 (6) 714-22.
Journal code: 0154720. ISSN: 0031-6768.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF171068
ENTRY MONTH: 200006
ENTRY DATE: Entered STN: 20000629
Last Updated on STN: 20000629
Entered Medline: 20000621

L2 ANSWER 53 OF 73 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2000:178435 BIOSIS
DOCUMENT NUMBER: PREV200000178435
TITLE: ***TREK*** -2, a new member of the mammalian mechanosensitive K+ channel family.
AUTHOR(S): Bang, Hyoweon (1); Kim, Yangmi (1); Kim, Donghee (1)
CORPORATE SOURCE: (1) Chicago Medical School, 3333 Green Bay Road, North
Chicago, IL, 60064 USA
SOURCE: Biophysical Journal, (Jan., 2000) Vol. 78, No. 1 Part 2, pp. 474A.
Meeting Info.: 44th Annual Meeting of the Biophysical Society. New Orleans, Louisiana, USA February 12-16, 2000
ISSN: 0006-3495.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L2 ANSWER 54 OF 73 MEDLINE DUPLICATE 34
ACCESSION NUMBER: 2000488784 MEDLINE
DOCUMENT NUMBER: 20492877 PubMed ID: 11039733
TITLE: Localization of the tandem pore domain K+ channel TASK-1 in
the rat central nervous system.
AUTHOR: Kindler C H; Pietruck C; Yost C S; Sampson E R; Gray A T
CORPORATE SOURCE: Department of Anesthesia, University of Basel, Kantonsspital, Switzerland.. ckindler@uhbs.ch
CONTRACT NUMBER: GMS-51372 (NIGMS)
SOURCE: BRAIN RESEARCH. MOLECULAR BRAIN RESEARCH, (2000 Aug 14) 80
(1) 99-108.
Journal code: 8908640. ISSN: 0169-328X.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200103
ENTRY DATE: Entered STN: 20010404
Last Updated on STN: 20010404
Entered Medline: 20010301

L2 ANSWER 55 OF 73 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.DUPLICATE
35
ACCESSION NUMBER: 2000:353891 BIOSIS
DOCUMENT NUMBER: PREV200000353891
TITLE: Expression of ***TREK*** -1 ***potassium*** ***channel*** in GABA-containing neurons in the adult rat
CNS.
AUTHOR(S): Cluderay, J. E. (1); Meadows, H. J. (1); Hervieu, G. (1)
CORPORATE SOURCE: (1) Neuroscience Research, SB, Harlow, Essex UK
SOURCE: European Journal of Neuroscience, (2000) Vol. 12, No. Supplement 11, pp. 23. print.
Meeting Info.: Meeting of the Federation of European Neuroscience Societies Brighton, UK June 24-28, 2000
ISSN: 0953-816X.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L2 ANSWER 56 OF 73 WPIDS (C) 2002 THOMSON DERWENT DUPLICATE 36
ACCESSION NUMBER: 1999-469126 [39] WPIDS
DOC. NO. NON-CPI: N1999-350285
DOC. NO. CPI: C1999-137655
TITLE: New two pore ***potassium*** ***channel*** used
for, e.g. treatment of cancer, pulmonary, cardiovascular and inflammatory diseases.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): CHAPMAN, C G; MEADOWS, H J
PATENT ASSIGNEE(S): (SMIK) SMITHKLINE BEECHAM PLC; (CHAP-I) CHAPMAN C G;
(MEAD-I) MEADOWS H J
COUNTRY COUNT: 21
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9937762	A1	19990729 (199939)*		EN	26

RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE
W: JP
EP 1051485 A1 20001115 (200059) EN
R: BE CH DE DK FR GB IT LI NL
US 6242217 B1 20010605 (200133)
US 2002028485 A1 20020307 (200221)
JP 2002511233 W 20020416 (200242) 52

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9937762	A1	WO 1998-EP7805	19981202
EP 1051485	A1	EP 1998-962402	19981202
		WO 1998-EP7805	19981202
US 6242217	B1	US 1999-236080	19990125
US 2002028485	A1 Div ex	US 1999-236080	19990125
		US 2001-828746	20010409
JP 2002511233	W	WO 1998-EP7805	19981202
		JP 2000-528670	19981202

FILING DETAILS:

PATENT NO	KIND	PATENT NO
EP 1051485	A1 Based on	WO 9937762
US 2002028485	A1 Div ex	US 6242217
JP 2002511233	W Based on	WO 9937762

PRIORITY APPLN. INFO: GB 1998-22135 19981009; EP 1998-300570
19980127

L2 ANSWER 57 OF 73 WPIDS (C) 2002 THOMSON DERWENT
ACCESSION NUMBER: 1999-551038 [46] WPIDS
DOC. NO. NON-CPI: N1999-407763
DOC. NO. CPI: C1999-160733
TITLE: New mechanically sensitive ***potassium*** ***channel*** , used to screen for specific modulators, potential therapeutic agents for heart and nervous system disorders.
DERWENT CLASS: B04 D16 S03
INVENTOR(S): DUPRAT, F; FINK, M; HONORE, E; LAZDUNSKI, M; LESAGE, F
PATENT ASSIGNEE(S): (CNRS) CNRS CENT NAT RECH SCI
COUNTRY COUNT: 21
PATENT INFORMATION:

PATENT NO	KIND	DATE	WEEK	LA	PG
WO 9945108	A2	19990910 (199946)*		FR	40

RW: AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE
W: CA JP US
FR 2775688 A1 19990910 (199946)
EP 1058726 A2 20001213 (200066) FR
R: DE ES FR GB IT
JP 2002505102 W 20020219 (200216) 41

APPLICATION DETAILS:

PATENT NO	KIND	APPLICATION	DATE
WO 9945108	A2	WO 1999-FR404	19990223
FR 2775688	A1	FR 1998-2725	19980305
EP 1058726	A2	EP 1999-904937	19990223
		WO 1999-FR404	19990223
JP 2002505102	W	WO 1999-FR404	19990223
		JP 2000-534640	19990223

FILING DETAILS:

PATENT NO	KIND	PATENT NO
EP 1058726	A2 Based on	WO 9945108
JP 2002505102	W Based on	WO 9945108

PRIORITY APPLN. INFO: FR 1998-2725 19980305

L2 ANSWER 58 OF 73 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1999:566066 CAPLUS
DOCUMENT NUMBER: 131:168355
TITLE: Identification of human genes for K+Hnov ***potassium*** ***channels*** by gene discovery methods and their investigative, diagnostic, and therapeutic uses
INVENTOR(S): Miller, Andrew P.; Curran, Mark Edward; Hu, Ping;
Rutter, Marc; Wang, Jian-ying
PATENT ASSIGNEE(S): Axys Pharmaceuticals, Inc., USA
SOURCE: PCT Int. Appl., 112 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9943696	A1	19990902	WO 1999-US3826	19990222

W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE,
DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP,
KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN,
MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM,
TR, TT, UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES,
FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI,
CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

CA 2321194	AA	19990902	CA 1999-2321194	19990222
AU 9927809	A1	19990915	AU 1999-27809	19990222
AU 747846	B2	20020523		
EP 1056765	A1	20001206	EP 1999-908356	19990222

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
IE, FI
US 6399761 B1 20020604 US 1999-336643 19990618
PRIORITY APPLN. INFO.: US 1998-76687P P 19980225
US 1998-95836P P 19980807
US 1999-116448P P 19990119
WO 1999-US3826 W 19990222
REFERENCE COUNT: 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 59 OF 73 MEDLINE DUPLICATE 37
ACCESSION NUMBER: 1999410397 MEDLINE
DOCUMENT NUMBER: 99410397 PubMed ID: 10480871
TITLE: Mechano- or acid stimulation, two interactive modes of activation of the ***TREK*** -1 ***potassium*** ***channel*** .
AUTHOR: Maingret F; Patel A J; Lesage F; Lazdunski M; Honore E
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire, CNRS
UPR 411, 660 route des Lucioles, Sophia Antipolis, 06560 Valbonne, France.
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1999 Sep 17) 274 (38)
26691-6.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Space Life Sciences

ENTRY MONTH: 199910
ENTRY DATE: Entered STN: 19991026
Last Updated on STN: 19991026
Entered Medline: 19991013

L2 ANSWER 60 OF 73 BIOSIS COPYRIGHT 2002 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2000:137222 BIOSIS
DOCUMENT NUMBER: PREV200000137222
TITLE: Cloning, localisation and functional expression of a novel human 2P domain ***potassium*** ***channel*** .
AUTHOR(S): Meadows, H. J. (1); Chapman, C. G.; Jennings, C. (1); Hervieu, G. (1); Cluderay, J. (1); Randall, A. R. (1); Gloger, I. S.; Benham, C. D. (1)
CORPORATE SOURCE: (1) Neuroscience, SmithKline Beecham Pharmaceuticals, Third
Avenue, New Frontiers Science Park North, Harlow, Essex, CM19 5AW UK
SOURCE: Society for Neuroscience Abstracts., (1999) Vol. 25, No.
1-2, pp. 2248.
Meeting Info.: 29th Annual Meeting of the Society for Neuroscience. Miami Beach, Florida, USA October 23-28, 1999
Society for Neuroscience
. ISSN: 0190-5295.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English

L2 ANSWER 61 OF 73 MEDLINE DUPLICATE 38
ACCESSION NUMBER: 1999098876 MEDLINE
DOCUMENT NUMBER: 99098876 PubMed ID: 9880510
TITLE: TRAAK is a mammalian neuronal mechano-gated K+ channel.
AUTHOR: Maingret F; Fosset M; Lesage F; Lazdunski M; Honore E
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire,
CNRS-UPR 411, 660 route des Lucioles, Sophia Antipolis, 06560 Valbonne, France.
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1999 Jan 15) 274 (3)
1381-7.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals; Space Life Sciences
ENTRY MONTH: 199902
ENTRY DATE: Entered STN: 19990223
Last Updated on STN: 19990223
Entered Medline: 19990211

L2 ANSWER 62 OF 73 MEDLINE DUPLICATE 39
ACCESSION NUMBER: 1999215865 MEDLINE
DOCUMENT NUMBER: 99215865 PubMed ID: 10201682
TITLE: Local anesthetic inhibition of baseline ***potassium*** ***channels*** with two pore domains in tandem.
AUTHOR: Kindler C H; Yost C S; Gray A T
CORPORATE SOURCE: Department of Anesthesia, University of California, San
Francisco 94143-0542, USA.
CONTRACT NUMBER: GMS-51372 (NIGMS)
SOURCE: ANESTHESIOLOGY, (1999 Apr) 90 (4) 1092-102.
Journal code: 1300217. ISSN: 0003-3022.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Abridged Index Medicus Journals; Priority Journals
ENTRY MONTH: 199904
ENTRY DATE: Entered STN: 19990504
Last Updated on STN: 19990504
Entered Medline: 19990421

L2 ANSWER 63 OF 73 MEDLINE DUPLICATE 40
ACCESSION NUMBER: 1999254548 MEDLINE
DOCUMENT NUMBER: 99254548 PubMed ID: 10321245
TITLE: Inhalational anesthetics activate two-pore-domain background K+ channels.
AUTHOR: Patel A J; Honore E; Lesage F; Fink M; Romey G; Lazdunski M
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire-CNRS-UPR 411, Valbonne, France.
SOURCE: NATURE NEUROSCIENCE, (1999 May) 2 (5) 422-6.
Journal code: 9809671. ISSN: 1097-6256.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199905
ENTRY DATE: Entered STN: 19990607
Last Updated on STN: 19990607
Entered Medline: 19990525

L2 ANSWER 64 OF 73 MEDLINE DUPLICATE 41
ACCESSION NUMBER: 1999103971 MEDLINE
DOCUMENT NUMBER: 99103971 PubMed ID: 9887061
TITLE: Potential identification of the O2-sensitive K+ current in a human neuroepithelial body-derived cell line.
AUTHOR: O'Kelly I; Stephens R H; Peers C; Kemp P J
CORPORATE SOURCE: School of Biomedical Sciences, University of Leeds, Leeds
LS2 9JT, United Kingdom.
SOURCE: AMERICAN JOURNAL OF PHYSIOLOGY, (1999 Jan) 276 (1 Pt 1)
L96-L104.
Journal code: 0370511. ISSN: 0002-9513.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199903
ENTRY DATE: Entered STN: 19990324
Last Updated on STN: 19990324
Entered Medline: 19990309

L2 ANSWER 65 OF 73 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 1999:85877 SCISEARCH
THE GENUINE ARTICLE: 158ED
TITLE: Potential identification of the O-2-sensitive K+ current in a human neuroepithelial body-derived cell line
AUTHOR: OKelly I; Stephens R H; Peers C; Kemp P J (Reprint)
CORPORATE SOURCE: UNIV LEEDS, SCH BIOMED SCI, WORSLEY MED & DENT BLDG, LEEDS
LS2 9JT, W YORKSHIRE, ENGLAND (Reprint); UNIV LEEDS, SCH
BIOMED SCI, LEEDS LS2 9JT, W YORKSHIRE, ENGLAND; UNIV
LEEDS, INST CARDIOVASC RES, LEEDS LS2 9JT, W YORKSHIRE,
ENGLAND
COUNTRY OF AUTHOR: ENGLAND
SOURCE: AMERICAN JOURNAL OF PHYSIOLOGY-LUNG CELLULAR AND MOLECULAR
PHYSIOLOGY, (JAN 1999) Vol. 20, No. 1, pp. L96-L104.
Publisher: AMER PHYSIOLOGICAL SOC, 9650 ROCKVILLE PIKE,
BETHESDA, MD 20814.
ISSN: 1040-0605.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: English
REFERENCE COUNT: 25
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

L2 ANSWER 66 OF 73 MEDLINE DUPLICATE 42
ACCESSION NUMBER: 1999030343 MEDLINE
DOCUMENT NUMBER: 99030343 PubMed ID: 9812978
TITLE: Cloning and expression of a novel pH-sensitive two pore domain K+ channel from human kidney.
AUTHOR: Reyes R; Duprat F; Lesage F; Fink M; Salinas M; Farman N;
Lazdunski M
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire,
CNRS-UPR 411, 660 route des Lucioles, Sophia Antipolis, 06560 Valbonne, France.
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1998 Nov 20) 273 (47)
30863-9.
Journal code: 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF084830
ENTRY MONTH: 199812
ENTRY DATE: Entered STN: 19990115
Last Updated on STN: 19990115
Entered Medline: 19981221

L2 ANSWER 67 OF 73 MEDLINE DUPLICATE 43
ACCESSION NUMBER: 1998353454 MEDLINE
DOCUMENT NUMBER: 98353454 PubMed ID: 9687497
TITLE: A mammalian two pore domain mechano-gated S-like K+ channel.
AUTHOR: Patel A J; Honore E; Maingret F; Lesage F; Fink M; Duprat
F; Lazdunski M
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire, CNRS,
Valbonne, France.
SOURCE: EMBO JOURNAL, (1998 Aug 3) 17 (15) 4283-90.
Journal code: 8208664. ISSN: 0261-4189.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199809
ENTRY DATE: Entered STN: 19981006
Last Updated on STN: 19981006
Entered Medline: 19980922

L2 ANSWER 68 OF 73 MEDLINE DUPLICATE 44
ACCESSION NUMBER: 1998292450 MEDLINE
DOCUMENT NUMBER: 98292450 PubMed ID: 9628867
TITLE: A neuronal two P domain K+ channel stimulated by arachidonic acid and polyunsaturated fatty acids.
AUTHOR: Fink M; Lesage F; Duprat F; Heurteaux C; Reyes R; Fosset M;
Lazdunski M
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire-CNRS-UPR 411, Valbonne, France.
SOURCE: EMBO JOURNAL, (1998 Jun 15) 17 (12) 3297-308.
Journal code: 8208664. ISSN: 0261-4189.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF056492
ENTRY MONTH: 199807
ENTRY DATE: Entered STN: 19980811
Last Updated on STN: 20000303
Entered Medline: 19980730

L2 ANSWER 69 OF 73 MEDLINE DUPLICATE 45
ACCESSION NUMBER: 1998099797 MEDLINE
DOCUMENT NUMBER: 98099797 PubMed ID: 9437008
TITLE: An open rectifier ***potassium*** ***channel*** with two pore domains in tandem cloned from rat cerebellum.
AUTHOR: Leonoudakis D; Gray A T; Winegar B D; Kindler C H; Harada
M; Taylor D M; Chavez R A; Forsayeth J R; Yost C S
CORPORATE SOURCE: Department of Anesthesia, University of California San
Francisco, San Francisco, California 94143-0542, USA.
CONTRACT NUMBER: GM-08440 (NIGMS)
GMS-51372 (NIGMS)
SOURCE: JOURNAL OF NEUROSCIENCE, (1998 Feb 1) 18 (3) 868-77.
Journal code: 8102140. ISSN: 0270-6474.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF031384
ENTRY MONTH: 199802
ENTRY DATE: Entered STN: 19980224
Last Updated on STN: 20000303
Entered Medline: 19980206

L2 ANSWER 70 OF 73 MEDLINE DUPLICATE 46
ACCESSION NUMBER: 1998165556 MEDLINE
DOCUMENT NUMBER: 98165556 PubMed ID: 9506712
TITLE: Cloning and functional expression of a novel cardiac two-pore background K+ channel (cTBAK-1).
AUTHOR: Kim D; Fujita A; Horio Y; Kurachi Y
CORPORATE SOURCE: Department of Pharmacology II, Faculty of Medicine, Osaka
University, Suita, Japan.
SOURCE: CIRCULATION RESEARCH, (1998 Mar 9) 82 (4) 513-8.
Journal code: 0047103. ISSN: 0009-7330.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AB008537
ENTRY MONTH: 199803
ENTRY DATE: Entered STN: 19980410
Last Updated on STN: 19980410
Entered Medline: 19980327

L2 ANSWER 71 OF 73 MEDLINE DUPLICATE 47
ACCESSION NUMBER: 1998389638 MEDLINE
DOCUMENT NUMBER: 98389638 PubMed ID: 9721223
TITLE: Mapping of human ***potassium*** ***channel*** genes ***TREK*** -1 (KCNK2) and TASK (KCNK3) to chromosomes 1q41 and 2p23.
AUTHOR: Lesage F; Lazdunski M
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire, CNRS,
Valbonne, 660 route des Lucioles, Sophia Antipolis, 06560, France.
SOURCE: GENOMICS, (1998 Aug 1) 51 (3) 478-9.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF006823
ENTRY MONTH: 199810
ENTRY DATE: Entered STN: 19981020
Last Updated on STN: 19981020
Entered Medline: 19981005

L2 ANSWER 72 OF 73 MEDLINE DUPLICATE 48
ACCESSION NUMBER: 97459932 MEDLINE
DOCUMENT NUMBER: 97459932 PubMed ID: 9312005
TITLE: TASK, a human background K+ channel to sense external pH
variations near physiological pH.
AUTHOR: Duprat F; Lesage F; Fink M; Reyes R; Heurteaux C; Lazdunski
M
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire, CNRS,
660 route des Lucioles, Sophia Antipolis, 06560 Valbonne, France.
SOURCE: EMBO JOURNAL, (1997 Sep 1) 16 (17) 5464-71.
Journal code: 8208664. ISSN: 0261-4189.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF006823; GENBANK-AF006824
ENTRY MONTH: 199712
ENTRY DATE: Entered STN: 19980109
Last Updated on STN: 19980109

Entered Medline: 19971215

L2 ANSWER 73 OF 73 MEDLINE DUPLICATE 49
ACCESSION NUMBER: 97157476 MEDLINE
DOCUMENT NUMBER: 97157476 PubMed ID: 9003761
TITLE: Cloning, functional expression and brain localization of a novel unconventional outward rectifier K+ channel.
AUTHOR: Fink M; Duprat F; Lesage F; Reyes R; Romey G; Heurteaux C; Lazdunski M
CORPORATE SOURCE: Institut de Pharmacologie Moleculaire et Cellulaire, CNRS, Valbonne, France.
SOURCE: EMBO JOURNAL, (1996 Dec 16) 15 (24) 6854-62. Journal code: 8208664. ISSN: 0261-4189.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U73488
ENTRY MONTH: 199702
ENTRY DATE: Entered STN: 19970227
Last Updated on STN: 19980206
Entered Medline: 19970213

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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: September 21, 2002, 05:44:09 ; Search time 3779.57 Seconds
(without alignments)
11433.390 Million cell updates/sec

Title: US-09-729-920-1
Perfect score: 2065
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
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9: gb_pr:*
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17: em_hum:*
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24: em_ph:*
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28: em_un:*
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30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	621.4	30.1	110939	9	CNS01DSW	AL122021 Human chr
5	621.4	30.1	191090	2	AP000927	AP000927 Homo sapi
c 6	621.4	30.1	197224	9	CNS01DUM	AL133279 Human chr
7	476	23.1	3187	10	AF325671	AF325671 Rattus no
8	469.6	22.7	3580	10	MMU73488	U73488 Mus musculu
9	468.2	22.7	1236	9	AF129399	AF129399 Homo sapi
10	468.2	22.7	1246	6	AR156458	AR156458 Sequence
11	468.2	22.7	1246	6	AX003047	AX003047 Sequence
12	468.2	22.7	1246	6	AX054800	AX054800 Sequence
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14	468	22.7	1993	6	AX018706	AX018706 Sequence
15	468	22.7	1994	6	AR156460	AR156460 Sequence
16	468	22.7	1994	6	AX003051	AX003051 Sequence
17	458.6	22.2	2130	6	AX224564	AX224564 Sequence
18	458.6	22.2	2130	6	AX224579	AX224579 Sequence
19	457.6	22.2	2106	9	AF004711	AF004711 Homo sapi
20	457	22.1	2130	6	AX224580	AX224580 Sequence
21	457	22.1	2130	6	AX224582	AX224582 Sequence
22	455.4	22.1	2130	6	AX224581	AX224581 Sequence
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28	279.2	13.5	1730	9	AF259500	AF259500 Homo sapi
29	279.2	13.5	2747	9	AF259501	AF259501 Homo sapi
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38	181	8.8	321	6	AX003049	AX003049 Sequence
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ALIGNMENTS

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DEFINITION Sequence 34 from Patent WO0185788.
ACCESSION AX319989
VERSION AX319989.1 GI:17901533
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Roberds,S.L., Benjamin,C.W., Karnovsky,A.M. and Ruble,C.L.
TITLE Human ion channels
JOURNAL Patent: WO 0185788-A 34 15-NOV-2001;
PHARMACIA & UPJOHN COMPANY (US)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
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BASE COUNT 405 a 423 c 463 g 341 t
ORIGIN

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  Matches 1631;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    554 gctccgactccaactccgcgcctgtccatttcctcccgagccacagtggtagccaggatg 613
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Db    181 GAAGGCACCTCCCAAGGGGGCTTGCAGACCGTCATGAAGTGGAAGACGGTGGTTGCCATC 240

Qy    674 tttgtggttgtggtggtctaccttgtcactggcggtcttgtcttccgggcattggagcag 733
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TTTGTGGTTGTGGTGGTCTACCTTGTCACTGGCGGTCTTGTCTTCCGGGCATTGGAGCAG 300

Qy    734 ccctttgagagcagccagaagaataccatcgccttggagaaggcggaattcctgcgggat 793
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Qy    794 catgtctgtgtgagcccccaggagctggagacgttgatccagcatgctcttgatgctgac 853
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Db    361 CATGTCTGTGTGAGCCCCCAGGAGCTGGAGACGTTGATCCAGCATGCTCTTGATGCTGAC 420

Qy    854 aatgcgggagtcagtccaataggaaactcttccaacaacagcagccactgggacctcggc 913
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Qy    914 agtgccttttttctttgctggaactgtcattacgaccatagggtatgggaatattgctccg 973
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Qy    974 agcactgaaggaggcaaaatcttttgtattttatatgccatctttggaattccactcttt 1033
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Qy   1094 agagtggagaaggtctttcgaaaaaagcaagtgagtcagaccaagatccgggtcatctca 1153
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Qy   1154 accatcctgttcatcttggccggctgcattgtgtttgtgacgatccctgctgtcatcttt 1213
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Qy   1454 atcaaggcccatgcggcagagtggaaggccaatgtcacggctgagttccgggagacacgg 1513
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Qy   1514 cgaaggctcagcgtggagatccacgataagctgcagcgggcggccaccatccgcagcatg 1573
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Qy   1634 aagcgctctgtctttgctgccctggacaccggccgcttcaaggcctcatcccaggagagc 1693
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Qy   1694 atcaacaaccggcccaacaacctgcgcctgaaggggccggagcagctgaacaagcatggg 1753
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Qy   1754 cagggtgcgtccgaggacaacatcatcaacaagttcgggtccacctccagactcaccaag 1813
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Qy   1814 aggaaaaacaaggacctcaaaaagaccttgcccgaggacgttcagaaaatctacaagacc 1873
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Qy   1874 ttccggaattactccctggacgaggagaagaaagaggaggaaacggaaaagatgtgtaac 1933
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Qy   1934 tcagacaactccagcacagccatgctgacggactgtatccagcagcacgctgagttggag 1993
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Qy   1994 aacggaatgatacccacggacaccaaagaccgggagccggagaacaactcattacttgaa 2053
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Db   1561 AACGGAATGATACCCACGGACACCAAAGACCGGGAGCCGGAGAACAACTCATTACTTGAA 1620

Qy   2054 gacagaaaactaa 2065
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Db   1621 GACAGAAACTAA 1632


RESULT   2
AF279890
LOCUS       AF279890               2730 bp    mRNA    linear   PRI 20-SEP-2000
DEFINITION  Homo sapiens 2P domain potassium channel TREK2 (KCNK10) mRNA,
            complete cds.
ACCESSION   AF279890
VERSION     AF279890.1  GI:10198114
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2730)
  AUTHORS   Lesage,F., Terrenoire,C., Romey,G. and Lazdunski,M.
  TITLE     Human TREK2, a 2P domain mechano-sensitive K+ channel with multiple
            regulations by polyunsaturated fatty acids, lysophospholipids, and
            gs, gi, and Gq protein-coupled receptors
  JOURNAL   J. Biol. Chem. 275 (37), 28398-28405 (2000)
  MEDLINE   20435789
REFERENCE   2  (bases 1 to 2730)
  AUTHORS   Lesage,F.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JUN-2000) IPMC, CNRS, 660 Route des Lucioles,
            Valbonne 06560, France
FEATURES             Location/Qualifiers
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                     /product="2P domain potassium channel TREK2"
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                     /db_xref="GI:10198115"
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                     AGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVE
                     KVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTT
                     VGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVLSMIGDWLRVLSKKTKEEVG
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                     SPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGPEQLNKHGQGASEDNIINKFGST
                     SRLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEEETEKMCNSDNSSTAMLTDCI
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BASE COUNT      658 a    680 c    772 g    620 t
ORIGIN
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Query Match 76.5%; Score 1579.4; DB 9; Length 2730;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1580; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db     509 GTGGCCGTTCCCGCAGCAGCACCGGTGTGCCAGCCCAAGAGCGCCACTAACGGGCAACCC 568

Qy     545 ccggctccggctccgactccaactccgcgcctgtccatttcctcccgagccacagtggta 604
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     569 CCGGCTCCGGCTCCGACTCCAACTCCGCGCCTGTCCATTTCCTCCCGAGCCACAGTGGTA 628

Qy     605 gccaggatggaaggcacctcccaaggggggcttgcagaccgtcatgaagtggaagacggtg 664
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Db     629 GCCAGGATGGAAGGCACCTCCCAAGGGGGCTTGCAGACCGTCATGAAGTGGAAGACGGTG 688

Qy     665 gttgccatctttgtggttgtggtggtctacccttgtcactggcggtcttgtcttccgggca 724
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Db     689 GTTGCCATCTTTGTGGTTGTGGTGGTCTACCTTGTCACTGGCGGTCTTGTCTTCCGGGCA 748

Qy     725 ttggagcagccctttgagagcagccagaagaataccatcgccttggagaaggcggaattc 784
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Db     749 TTGGAGCAGCCCTTTGAGAGCAGCCAGAAGAATACCATCGCCTTGGAGAAGGCGGAATTC 808

Qy     785 ctgcgggatcatgtctgtgtgagcccccaggagctggagacgttgatccagcatgctctt 844
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Db     809 CTGCGGGATCATGTCTGTGTGAGCCCCCAGGAGCTGGAGACGTTGATCCAGCATGCTCTT 868

Qy     845 gatgctgacaatgcgggagtcagtccaataggaaactcttccaacaacagcagccactgg 904
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Db     869 GATGCTGACAATGCGGGAGTCAGTCCAATAGGAAACTCTTCCAACAACAGCAGCCACTGG 928

Qy     905 gacctcggcagtgccttttttctttgctggaactgtcattacgaccatagggtatgggaat 964
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Qy     965 attgctccgagcactgaaggaggcaaaatcttttgtattttatatgccatctttggaatt 1024
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Qy    1025 ccactctttggtttcttattggctggaattggagaccaacttggaaccatctttgggaaa 1084
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Db    1049 CCACTCTTTGGTTTCTTATTGGCTGGAATTGGAGACCAACTTGGAACCATCTTTGGGAAA 1108

Qy    1085 agcattgcaagagtggagaaggtctttcgaaaaaagcaagtgagtcagaccaagatccgg 1144
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Qy    1145 gtcatctcaaccatcctgttcatcttggccggctgcattgtgtttgtgacgatccctgct 1204
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Qy    1205 gtcatctttaagtacatcgagggctggacggccttggagtccatttactttgtggtggtc 1264
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Qy    1625 tcccccgagaagcgctctgtctttgctgccctggacaccggccgcttcaaggcctcatcc 1684
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Qy    1685 caggagagcatcaacaaccggcccaacaacctgcgcctgaaggggccggagcagctgaac 1744
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Qy    1745 aagcatgggcagggtgcgtccgaggacaacatcatcaacaagttcgggtccacctccaga 1804
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Qy    1805 ctcaccaagaggaaaaacaaggacctcaaaaagaccttgcccgaggacgttcagaaaatc 1864
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RESULT   3
AF196965
LOCUS       AF196965               1854 bp    mRNA    linear   ROD 11-JUN-2000
DEFINITION  Rattus norvegicus potassium channel TREK-2 mRNA, complete cds.
ACCESSION   AF196965
VERSION     AF196965.1  GI:8452899
KEYWORDS    .
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
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            Rattus.
REFERENCE   1  (bases 1 to 1854)
  AUTHORS   Bang,H., Kim,Y. and Kim,D.
  TITLE     TREK-2, a new member of the mechanosensitive tandem-pore K+ channel
            family
  JOURNAL   J. Biol. Chem. 275 (23), 17412-17419 (2000)
  MEDLINE   20298807
REFERENCE   2  (bases 1 to 1854)
  AUTHORS   Kim,D. and Bang,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-OCT-1999) Physiology and Biophysics, Finch University
            of Health Sciences/The Chicago Medical School, 3333 Green Bay Road,
            North Chicago, IL 60064, USA
FEATURES             Location/Qualifiers
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BASE COUNT      485 a    448 c    478 g    443 t
ORIGIN
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  Best Local Similarity   87.7%;  Pred. No. 9.2e-309;
  Matches 1587;  Conservative    0;  Mismatches  197;  Indels   26;  Gaps    6;

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Qy    323 cccatcctcggaaattgttttgttggactgctaaaccgaggcg-tgtaaagcttgaggac 381
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Qy    382 tttatta--ttatttgggttcttttcatttc-ttccccttctgggcaacgaagcaatgaa 438
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Qy    439 atttccaatcgagacgccaagaaaacaggtgaactgggatcctaaagtggccgttcccgc 498
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Qy    499 agcag---caccggtgtgccagcccaagagcgccactaacgggcaacccccggctccggc 555
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Qy    556 tccgactccaactccgcgcctgtccatttcctcccgagccacagtggtagccaggatgga 615
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Qy    616 aggcacctcccaaggggcttgcagaccgtcatgaagtggaagacggtggttgccatctt 675
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Qy    676 tgtggttgtggtggtctaccttgtcactggcggtcttgtcttccgggcattggagcagcc 735
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Db    404 TGTGGTGGTCGTGGTCTACCTCGTCACCGGTGGCCTTGTCTTCCGGGCATTGGAACAGCC 463

Qy    736 ctttgagagcagccagaagaataccatcgccttggagaaggcggaattcctgcgggatca 795
          |||||||||||| |||||||| || || ||||||||||||||| |||||| || | |||||
Db    464 CTTTGAGAGCAGTCAGAAGAACACAATTGCCTTGGAGAAGGCAGAATTCTTGAGAGATCA 523

Qy    796 tgtctgtgtgagcccccaggagctggagacgttgatccagcatgctcttgatgctgacaa 855
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Db    524 TATCTGTGTGAGCCCCCAGGAACTGGAGACACTGATCCAGCACGCACTTGATGCTGATAA 583

Qy    856 tgcgggagtcagtccaataggaaactcttccaacaacagcagccactgggacctcggcag 915
          ||| || ||||| ||  |||||||||| ||||||| |||||| |||||||||||||| ||
Db    584 TGCAGGGGTCAGCCCGGTAGGAAACTCCTCCAACAGCAGCAGTCACTGGGACCTCGGAAG 643

Qy    916 tgccttttttctttgctggaactgtcattacgaccatagggtatgggaatattgctccgag 975
          |||||| |||||||||| || ||||| ||||||||||||||||||||||||||||||||||
Db    644 TGCCTTCTTCTTTGCTGGGACGGTCATCACGACCATAGGGTATGGGAATATTGCTCCGAG 703

Qy    976 cactgaaggaggcaaaatcttttgtattttatatgccatctttggaattccactctttgg 1035
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Qy   1036 tttcttattggctggaattggagaccaacttggaaccatctttgggaaaagcattgcaag 1095
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Qy   1096 agtggagaaggtctttcgaaaaaagcaagtgagtcagaccaagatccgggtcatctcaac 1155
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Db    824 AGTGGAAAAGGTTTTCCGAAAAAAGCAAGTGAGTCAGACCAAGATCCGGGTCATCTCAAC 883

Qy   1156 catcctgttcatcttggccggctgcattgtgtttgtgacgatccctgctgtcatctttaa 1215
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Qy   1216 gtacatcgagggctggacggccttggagtccatttactttgtggtggtcactctgaccac 1275
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Qy   1276 ggtgggctttggtgattttgtggcaggggggaaacgctggcatcaattatcgggagtggta 1335
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Qy   1336 taagcccctagtgtggttttggatccttgttggccttgcctactttgcagctgtcctcag 1395
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Qy   1396 tatgatcggagattggctacgggttctgtccaaaaagacaaaagaagaggtgggtgaaat 1455
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Db   1124 TATGATTGGAGACTGGCTGCGAGTTTTATCCAAAAAGACAAAAGAAGAGGTGGGTGAGAT 1183

Qy   1456 caaggcccatgcggcagagtggaaggccaatgtcacggctgagttccgggagacacggcg 1515
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Db   1184 CAAAGCCCATGCAGCTGAATGGAAGGCTAATGTCACTGCTGAGTTCCGGGAGACGAGACG 1243

Qy   1516 aaggctcagcgtggagatccacgataagctgcagcgggcggccaccatccgcagcatgga 1575
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Db   1244 ACGGCTCAGCGTTGAGATCCATGACAAGCTGCAACGGGCAGCCACCATCCGAAGTATGGA 1303

Qy   1576 gcgccggcggctgggcctggaccagcgggcccactcactggacatgctgtcccccgagaa 1635
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Db   1304 GCGCCGGAGACTGGGATTGGACCAGAGGGCCCACTCACTGGACATGCTTTCCCCCGAGAA 1363

Qy   1636 gcgctctgtctttgctgccctggacaccggccgcttcaaggcctcatcccaggagagcat 1695
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Db   1364 GCGCTCTGTCTTTGCAGCCCTGGACACAGGCCGTTTCAAGGCCTCATCCCAGGAGAGTAT 1423

Qy   1696 caacaaccggcccaacaacctgcgcctgaaggggccggagcagctgaacaagcatgggca 1755
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Db   1424 CAACAACAGACCCAATAACCTACGCCTTAAGGGGCCAGAACAGCTCAACAAACACGGGCA 1483

Qy   1756 gggtgcgtccgaggacaacatcatcaacaagttcgggtccacctccagactcaccaagag 1815
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Db   1484 GGGCGCTTCTGAGGACAACATCATCAACAAGTTTGGGTCCACCTCCAAACTCACAAAGAG 1543
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Db   1544 GAAAAACAAAGATCTCAAAAAGACCTTACCTGAGGATGTTCAGAAAATCTACAAAACCTT 1603

Qy   1876 ccggaattactccctggacgaggagaagaaagaggaggaaacggaaaagatgtgtaactc 1935
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Db   1604 CCGGAATTACTCTCTGGATGAAGAGAAGAAAGAGGACGAGACAGAGAAGATGTGTAACTC 1663

Qy   1936 agacaactccagcacagccatgctgacggactgtatccagcagcacgctgagttggagaa 1995
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Db   1664 AGACAACTCCAGCACAGCCATGCTGACAGAGTGCATACAGCAGCAAGCTGAGATGGAGAA 1723

Qy   1996 cggaatgatacccacggacaccaaagaccgggagccggagaacaactcattacttgaaga 2055
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Db   1724 TGGAATGGTACCCATGGACACCAAAGACCAGGGGCTGGAGAACAATTCTTTACTTGAAGA 1783

Qy   2056 cagaaactaa 2065
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Db   1784 CAGAAACTAA 1793


RESULT   4
CNS01DSW
LOCUS       CNS01DSW              110939 bp    DNA     linear   PRI 24-MAY-2000
DEFINITION  Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC C-2365J20
            of library CalTech-D from chromosome 14 of Homo sapiens (Human),
            complete sequence.
ACCESSION   AL122021
VERSION     AL122021.3  GI:6434635
KEYWORDS    HTG; HTGS_DRAFT.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 110939)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-MAY-2000) to the EMBL/GenBank/DDBJ databases
COMMENT     On Nov 15, 1999 this sequence version replaced gi:6224506.
            IMPORTANT: This sequence is unfinished and does not necessarily
            represent the correct sequence. Work on the sequence is in progress
            and the release of this data is based on the understanding that the
            sequence may change as work continue. The sequence may be
            contaminated with foreign sequence from E.coli, yeast, vector,
            phage, etc. . . even if efforts are made to eliminate these
            contaminating sequences. The following BAC sequence is oriented
            from the T7 to the SP6 end.
            ----------------------
            Overall quality chart :
            Range    :   bases
            0        :
            1  -  9  :     424
            10 - 19  :    1599
            20 - 29  :    3896
            30 - 39  :   11020
            40 - 49  :    9524
            50 - 59  :   16929
            60 - 69  :   27035
            70 - 79  :   27734
            80 - 89  :   10322
            90 - 99  :    2456
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            Percentage of bases with a quality value >= 40 : 84 %.
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                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /clone="C-2365J20"
                     /clone_lib="CalTech-D"
BASE COUNT    29679 a  23251 c  25173 g  32836 t
ORIGIN
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  Best Local Similarity   99.8%;  Pred. No. 1.4e-132;
  Matches  622;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   1443 aggtgggtgaaatcaaggcccatgcggcagagtggaaggccaatgtcacggctgagttcc 1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 104770 AGGTGGGTGAAATCAAGGCCCATGCGGCAGAGTGGAAGGCCAATGTCACGGCTGAGTTCC 104829

Qy   1503 gggagacacggcgaaggctcagcgtggagatccacgataagctgcagcgggcggccacca 1562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 104830 GGGAGACACGGCGAAGGCTCAGCGTGGAGATCCACGATAAGCTGCAGCGGGCGGCCACCA 104889

Qy   1563 tccgcagcatggagcgccggcggctgggcctggaccagcgggcccactcactggacatgc 1622
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Db 104890 TCCGCAGCATGGAGCGCCGGCGGCTGGGCCTGGACCAGCGGGCCCACTCACTGGACATGC 104949

Qy   1623 tgtcccccgagaagcgctctgtctttgctgccctggacaccggccgcttcaaggcctcat 1682
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Db 104950 TGTCCCCCGAGAAGCGCTCTGTCTTTGCTGCCCTGGACACCGGCCGCTTCAAGGCCTCAT 105009

Qy   1683 cccaggagagcatcaacaaccggcccaacaacctgcgcctgaaggggccggagcagctga 1742
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Db 105010 CCCAGGAGAGCATCAACAACCGGCCCAACAACCTGCGCCTGAAGGGGCCGGAGCAGCTGA 105069

Qy   1743 acaagcatgggcagggtgcgtccgaggacaacatcatcaacaagttcgggtccacctcca 1802
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Db 105070 ACAAGCATGGGCAGGGTGCGTCCGAGGACAACATCATCAACAAGTTCGGGTCCACCTCCA 105129

Qy   1803 gactcaccaagaggaaaaacaaggacctcaaaaagaccttgcccgaggacgttcagaaaa 1862
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 105130 GACTCACCAAGAGGAAAAACAAGGACCTCAAAAAGACCTTGCCCGAGGACGTTCAGAAAA 105189

Qy   1863 tctacaagaccttccggaattactccctggacgaggagaagaaagaggaggaaacggaaa 1922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db 105190 TCTACAAGACCTTCCGGAATTACTCCCTGGACGAGGAGAAGAAAGAGGAGGAGACGGAAA 105249

Qy   1923 agatgtgtaactcagacaactccagcacagccatgctgacggactgtatccagcagcacg 1982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 105250 AGATGTGTAACTCAGACAACTCCAGCACAGCCATGCTGACGGACTGTATCCAGCAGCACG 105309

Qy   1983 ctgagttggagaacggaatgatacccacggacaccaaagaccgggagccggagaacaact 2042
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Db 105310 CTGAGTTGGAGAACGGAATGATACCCACGGACACCAAAGACCGGGAGCCGGAGAACAACT 105369

Qy   2043 cattacttgaagacagaaactaa 2065
          |||||||||||||||||||||||
Db 105370 CATTACTTGAAGACAGAAACTAA 105392


RESULT   5
AP000927
LOCUS       AP000927              191090 bp    DNA     linear   HTG 30-MAY-2000
DEFINITION  Homo sapiens chromosome 18 clone RP11-771O8 map 18p11.3, WORKING
            DRAFT SEQUENCE, 24 unordered pieces.
ACCESSION   AP000927
VERSION     AP000927.2  GI:8119068
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens DNA, clone:RP11-771O8.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 191090)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Homo sapiens 191,090 genomic DNA of 18p11.3
  JOURNAL   Published Only in DataBase (1999) In press
REFERENCE   2  (bases 1 to 191090)
  AUTHORS   Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
            Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-DEC-1999) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
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            Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
            Japan (E-mail:hattori@gsc.riken.go.jp,
            URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
            Fax:81-42-778-9924)
COMMENT     On May 31, 2000 this sequence version replaced gi:6997743.
            -------------- Genome Center
                Center: RIKEN Genomic Sciences Center(GSC)
                Center code: RIKEN
                Web site: http://hgp.gsc.riken.go.jp/
                Contact: hattori@gsc.riken.go.jp
            -------------- Project Information
                Center project name: HumDraft18
                Center clone name: RP11-771O8
            -------------- Summary Statistics
                Sequencing vector: PCR products; 100% of reads
                Chemistry: Dye-terminator ET-amersham; 100% of reads
                Assembly program: Phrap; version 0.990329
                Consensus quality: 175036 bases at least Q40
                Consensus quality: 182626 bases at least Q30
                Consensus quality: 186234 bases at least Q20
                Insert size: 188790; sum-of-contigs
                Quality coverage: 4.68x in Q20 bases; sum-of-contigs
            --------------.
            NOTE: This is a 'working draft' sequence. It currently consists of
            24 contigs. The true order of the pieces is not known and their
            order in this sequence record is arbitrary. Gaps between the
            contigs are represented as runs N, but the exact sizes of the gaps
            are unknown. This record will be updated with the finished sequence
            as soon as it is available and the accession number will be
            preserved
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              26685     48988 contig of  22304 bp in length
              49089     64798 contig of  15710 bp in length
              64899     80877 contig of  15979 bp in length
              80978     94387 contig of  13410 bp in length
              94488    108131 contig of  13644 bp in length
             108232    115507 contig of   7276 bp in length
             115608    125425 contig of   9818 bp in length
             125526    136206 contig of  10681 bp in length
             136307    144932 contig of   8626 bp in length
             145033    152815 contig of   7783 bp in length
             152916    157857 contig of   4942 bp in length
             157958    162888 contig of   4931 bp in length
             162989    166526 contig of   3538 bp in length
             166627    169154 contig of   2528 bp in length
             169255    172774 contig of   3520 bp in length
             172875    176556 contig of   3682 bp in length
             176657    179663 contig of   3007 bp in length
             179764    181210 contig of   1447 bp in length
             181311    183689 contig of   2379 bp in length
             183790    185492 contig of   1703 bp in length
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             189562    191090 contig of   1529 bp in length
            Sequence updated (26-May-2000).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 24 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
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            *   49089    64798: contig of 15710 bp in length
            *   64799 64898: gap of      100 bp
            *   64899    80877: contig of 15979 bp in length
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            *   94488   108131: contig of 13644 bp in length
            *  108132 108231: gap of      100 bp
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            *  115608   125425: contig of 9818 bp in length
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            *  144933 145032: gap of      100 bp
            *  145033   152815: contig of 7783 bp in length
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            *  183690 183789: gap of      100 bp
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            *  187966 188065: gap of      100 bp
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BASE COUNT    52517 a  41009 c  41120 g  54142 t   2302 others
ORIGIN


  Query Match             30.1%;  Score 621.4;  DB 2;  Length 191090;
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  Matches  622;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy    1443 aggtgggtgaaatcaaggcccatgcggcagagtggaaggccaatgtcacggctgagttcc 1502
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Db   60516 AGGTGGGTGAAATCAAGGCCCATGCGGCAGAGTGGAAGGCCAATGTCACGGCTGAGTTCC 60575

Qy    1503 gggagacacggcgaaggctcagcgtggagatccacgataagctgcagcgggcggccacca 1562
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Qy    1563 tccgcagcatggagcgccggcggctgggcctggaccagcgggcccactcactggacatgc 1622
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Qy    1623 tgtcccccgagaagcgctctgtctttgctgccctggacaccggccgcttcaaggcctcat 1682
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Db   60696 TGTCCCCCGAGAAGCGCTCTGTCTTTGCTGCCCTGGACACCGGCCGCTTCAAGGCCTCAT 60755

Qy    1683 cccaggagagcatcaacaaccggcccaacaacctgcgcctgaaggggccggagcagctga 1742
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Qy    1803 gactcaccaagaggaaaaacaaggacctcaaaaagaccttgcccgaggacgttcagaaaa 1862
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   60876 GACTCACCAAGAGGAAAAACAAGGACCTCAAAAAGACCTTGCCCGAGGACGTTCAGAAAA 60935

Qy    1863 tctacaagaccttccggaattactccctggacgaggagaagaaagaggaggaaacggaaa 1922
           |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db   60936 TCTACAAGACCTTCCGGAATTACTCCCTGGACGAGGAGAAGAAAGAGGAGGAGACGGAAA 60995

Qy    1923 agatgtgtaactcagacaactccagcacagccatgctgacggactgtatccagcagcacg 1982
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   60996 AGATGTGTAACTCAGACAACTCCAGCACAGCCATGCTGACGGACTGTATCCAGCAGCACG 61055

Qy    1983 ctgagttggagaacggaatgatacccacggacaccaaagaccgggagccggagaacaact 2042
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61056 CTGAGTTGGAGAACGGAATGATACCCACGGACACCAAAGACCGGGAGCCGGAGAACAACT 61115

Qy    2043 cattacttgaagacagaaactaa 2065
           |||||||||||||||||||||||
Db   61116 CATTACTTGAAGACAGAAACTAA 61138


RESULT   6
```

```
CNS01DUM/c
LOCUS       CNS01DUM              197224 bp    DNA     linear   PRI 26-APR-2001
DEFINITION  Human chromosome 14 DNA sequence BAC R-753D20 of library RPCI-11
            from chromosome 14 of Homo sapiens (Human), complete sequence.
ACCESSION   AL133279
VERSION     AL133279.7  GI:13513078
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 197224)
  AUTHORS   Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P.,
            Brottier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F.,
            Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,C.,
            Gyapay,G., Saurin,W. and Weissenbach,J.
  TITLE     Sequencing of the human chromosome 14
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 197224)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-APR-2001) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     On Apr 2, 2001 this sequence version replaced gi:12733870.
            -------------- Genome Center
            Center: Genoscope / Centre National de Sequencage
            Center code: GS
            Web site: http://www.genoscope.cns.fr/
            Contact: SeqRef@genoscope.cns.fr
            --------------
            The following BAC sequence is oriented from the T7 to the SP6 end.
            Upstream BAC (overlapping the T7 end) : R-300J18
            Downstream BAC (overlapping the SP6 end) : R-556K1 (AC=AL049834)
            -------------- Summary Statistics
            Assembly program: Phrap; version 2.0
            Quality coverage: 4.36x in Q20 bases; sum-of-contigs
            --------------
            ----------------------
            Overall quality chart :
            Range     :   bases
            0         :
            1   -  9  :
            10  - 19  :       5
            20  - 29  :      29
            30  - 39  :     435
            40  - 49  :    4625
            50  - 59  :   10185
            60  - 69  :   16319
            70  - 79  :   37578
            80  - 89  :   72140
            90  - 99  :   55908
            ----------------------
            Percentage of bases with a quality value >= 40 : 99 %.
FEATURES             Location/Qualifiers
     source          1. .197224
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /clone="R-753D20"
                     /clone_lib="RPCI-11"
     STS             19863. .19994
                     /note="matching EMBL:G19379
                     RHdb:RH14329
                     dbSTS:STS25998
                     Identified using the e-PCR software (G. Schuler)"
     STS             62917. .63074
                     /note="matching EMBL:Z16727
                     RHdb:RH53861
                     RHdb:RH15130
                     RHdb:RH9470
                     RHdb:RH3750
                     dbSTS:STS17284
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                Identified using the e-PCR software (G. Schuler)"
     STS        68831. .69007
                /note="matching EMBL:AA478101
                RHdb:RH104056
                dbSTS:STS71585
                Identified using the e-PCR software (G. Schuler)"
     STS        81607. .81746
                /note="matching EMBL:R38357
                RHdb:RH76689
                dbSTS:STS53776
                Identified using the e-PCR software (G. Schuler)"
     STS        83334. .83594
                /note="matching EMBL:Z51656
                RHdb:RH31323
                dbSTS:STS18406
                Identified using the e-PCR software (G. Schuler)"
     STS        84906. .85180
                /note="matching EMBL:Z38660
                RHdb:RH53866
                dbSTS:STS42912
                Identified using the e-PCR software (G. Schuler)"
BASE COUNT    57632 a  43838 c  40838 g  54916 t
ORIGIN
```

```
  Query Match           30.1%;  Score 621.4;  DB 9;  Length 197224;
  Best Local Similarity   99.8%;  Pred. No. 1.5e-132;
  Matches  622;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   1443 aggtgggtgaaatcaaggcccatgcggcagagtggaaggccaatgtcacggctgagttcc 1502
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  87640 AGGTGGGTGAAATCAAGGCCCATGCGGCAGAGTGGAAGGCCAATGTCACGGCTGAGTTCC 87581

Qy   1503 gggagacacggcgaaggctcagcgtggagatccacgataagctgcagcgggcggccacca 1562
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  87580 GGGAGACACGGCGAAGGCTCAGCGTGGAGATCCACGATAAGCTGCAGCGGGCGGCCACCA 87521

Qy   1563 tccgcagcatggagcgccggcggctgggcctggaccagcgggcccactcactggacatgc 1622
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  87520 TCCGCAGCATGGAGCGCCGGCGGCTGGGCCTGGACCAGCGGGCCCACTCACTGGACATGC 87461

Qy   1623 tgtcccccgagaagcgctctgtctttgctgccctggacaccggccgcttcaaggcctcat 1682
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  87460 TGTCCCCCGAGAAGCGCTCTGTCTTTGCTGCCCTGGACACCGGCCGCTTCAAGGCCTCAT 87401

Qy   1683 cccaggagagcatcaacaaccggcccaacaacctgcgcctgaaggggccggagcagctga 1742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  87400 CCCAGGAGAGCATCAACAACCGGCCCAACAACCTGCGCCTGAAGGGGCCGGAGCAGCTGA 87341

Qy   1743 acaagcatgggcagggtgcgtccgaggacaacatcatcaacaagttcgggtccacctcca 1802
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  87340 ACAAGCATGGGCAGGGTGCGTCCGAGGACAACATCATCAACAAGTTCGGGTCCACCTCCA 87281

Qy   1803 gactcaccaagaggaaaaacaaggacctcaaaaagaccttgcccgaggacgttcagaaaa 1862
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  87280 GACTCACCAAGAGGAAAAACAAGGACCTCAAAAAGACCTTGCCCGAGGACGTTCAGAAAA 87221

Qy   1863 tctacaagaccttccggaattactccctggacgaggagaagaaagaggaggaaacggaaa 1922
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  87220 TCTACAAGACCTTCCGGAATTACTCCCTGGACGAGGAGAAGAAAGAGGAGGAGACGGAAA 87161

Qy   1923 agatgtgtaactcagacaactccagcacagccatgctgacggactgtatccagcagcacg 1982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  87160 AGATGTGTAACTCAGACAACTCCAGCACAGCCATGCTGACGGACTGTATCCAGCAGCACG 87101

Qy   1983 ctgagttggagaacggaatgatacccacggacaccaaagaccgggagccggagaacaact 2042
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  87100 CTGAGTTGGAGAACGGAATGATACCCACGGACACCAAAGACCGGGAGCCGGAGAACAACT 87041

Qy   2043 cattacttgaagacagaaactaa 2065
          |||||||||||||||||||||||
Db  87040 CATTACTTGAAGACAGAAACTAA 87018
```

```
RESULT   7
AF325671
LOCUS       AF325671               3187 bp    mRNA    linear   ROD 08-SEP-2001
DEFINITION  Rattus norvegicus 2P domain potassium channel KCNK2 mRNA, complete
            cds.
ACCESSION   AF325671
VERSION     AF325671.1  GI:15528824
KEYWORDS    .
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 3187)
  AUTHORS   Bockenhauer,D., Zilberberg,N. and Goldstein,S.A.
  TITLE     KCNK2: reversible conversion of a hippocampal potassium leak into a
            voltage-dependent channel
  JOURNAL   Nat. Neurosci. 4 (5), 486-491 (2001)
  MEDLINE   21219399
   PUBMED   11319556
REFERENCE   2  (bases 1 to 3187)
  AUTHORS   Bockenhauer,D. and Goldstein,S.A.N.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-DEC-2000) Pediatrics, Section of Developmental
            Biology and Biophysics, Yale University Medical School, Boyer
            Center for Molecular Medicine, 295 Congress Avenue, New Haven, CT
            06536, USA
FEATURES             Location/Qualifiers
     source          1. .3187
                     /organism="Rattus norvegicus"
                     /db_xref="taxon:10116"
                     /tissue_type="brain"
     CDS             44. .1324
                     /note="similar to product encoded by Genbank accession
                     number AF065163"
                     /codon_start=1
                     /product="2P domain potassium channel KCNK2"
                     /protein_id="AAL01159.1"
                     /db_xref="GI:15528825"
                     /translation="MLASASRERPGYTAGVAAPDLLDPKSAAQNSKPRLSFSAKPTVL
                     ASRVESDSAINVMKWKTVSTIFLVVVLYLIIGATVFKALEQPQEISQRTTIVIQKQNF
                     IAQHACVNSTELDELIQQIVTAINAGIIPLGNNSNQVSHWDLGSSFFFAGTVITTIGF
                     GNISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQ
                     TKIRIISTIIFILFGCVLFVALPAVIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGG
                     SDIEYLDFYKPVVWFWILVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHAAEWTA
                     NVTAEFKETRRRLSVEIYDKFQRATSVKRKLSAELAGNHNQELTPCRRTLSVNHLTSE
                     REVLPPLLKAESIYLNGLTPHCAAEDIAVIENMK"
BASE COUNT      829 a    761 c    786 g    811 t
ORIGIN
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  Query Match           23.1%;  Score 476;  DB 10;  Length 3187;
  Best Local Similarity   67.9%;  Pred. No. 3.1e-99;
  Matches  697;  Conservative    0;  Mismatches  320;  Indels    9;  Gaps    2;

Qy    538 gcaaccccggctccggctccgactccaactccgcgcctgtccatttcctcccgagccac 597
          | | |||  | || | |||| ||   | |  ||| | || ||  | ||| |   | ||||
Db    109 GGATCCCAAGTCTGCTGCTCAGAACTCCAAACCGAGGCTCTCGTTCTCCGCAAAACCCAC 168

Qy    598 agtggtagccaggatggaaggcacctcccaaggggcttgcagaccgtcatgaagtggaa 657
           ||| | ||      ||  |  |    |   |          |  || ||||| |||||
Db    169 CGTGCTTGCTTCCCGGGTGGAGAGTGACTCGG------CCATTAATGTTATGAAATGGAA 222

Qy    658 gacggtggttgccatctttgtggttgtggtggtctaccttgtcactggcggtcttgtctt 717
          ||||||     | || ||  |||| || ||  |||||||  |||  || |     || ||
Db    223 GACGGTCTCCACGATTTTCCTGGTGGTCGTCCTCTACCTGATCATCGGAGCCACGGTGTT 282

Qy    718 ccgggcattggagcagccctttgagagcagccagaagaataccatcgccttggagaaggc 777
          |  ||| ||||||||||     ||||     |||| ||  ||||| |   |  ||||
Db    283 CAAGGCGTTGGAGCAGCCTCAGGAGATTTCTCAGAGGACCACCATTGTGATCCAGAAACA 342

Qy    778 ggaattcctgcgggatcatgtctgtgtgagcccccaggagctggagacgttgatccagca 837
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Db    343 GAACTTCATAGCCCAGCATGCCTGCGTCAACTCCACCGAGCTGGATGAACTCATCCAGCA 402

Qy    838 tgctcttgatgctgacaatgcgggagtcagtccaataggaaactcttccaacaacagcag 897
Db    403 AATAGTGACGGCCATAAATGCAGGGATTATCCCCTTAGGAAACAACTCCAATCAAGTTAG 462

Qy    898 ccactgggacctcggcagtgccttttttctttgctggaactgtcattacgaccatagggta 957
Db    463 TCACTGGGACCTCGGAAGCTCTTTCTTCTTTGCCGGCACTGTTATCACAACCATAGGATT 522

Qy    958 tgggaatattgctccgagcactgaaggaggcaaaatcttttgtattttatatgccatctt 1017
Db    523 TGGAAACATCTCCCCACGAACTGAAGGTGGAAAAATATTCTGTATCATCTATGCCTTGCT 582

Qy   1018 tggaattccactctttggtttcttattggctggaattggagaccaacttggaaccatctt 1077
Db    583 GGGAATTCCCCTCTTTGGTTTTCTACTGGCTGGGGTTGGGGATCAGCTTGGAACCATATT 642

Qy   1078 tgggaaaagcattgcaagagtggagaaggtctttcgaaaaaagcaagtgagtcagaccaa 1137
Db    643 TGGAAAAGGAATTGCCAAAGTGGAGGACACATTTATTAAGTGGAATGTTAGTCAGACCAA 702

Qy   1138 gatccgggtcatctcaaccatcctgttcatcttggccggctgcattgtgtttgtgacgat 1197
Db    703 GATTCGTATCATCTCGACCATCATCTTCATCCTGTTTGGCTGTGTCCTCTTCGTGGCTCT 762

Qy   1198 ccctgctgtcatctttaagtacatcgagggctggacggccttggagtccatttactttgt 1257
Db    763 CCCCGCCGTCATATTCAAGCACATAGAAGGCTGGAGTGCCCTGGACGCCATCTACTTTGT 822

Qy   1258 ggtggtcactctgaccacggtgggctttggtgattttgtggcaggggaaacgctggcat 1317
Db    823 GGTCATCACTCTGACCACCATTGGATTTGGCGATTATGTGGCAGGTGG---GTCGGACAT 879

Qy   1318 caattatcgggagtggtataagcccctagtgtggttttggatccttgttggccttgccta 1377
Db    880 TGAATATCTGGACTTCTACAAGCCCGTCGTGTGGTTCTGGATCCTCGTTGGGCTGGCCTA 939

Qy   1378 ctttgcagctgtcctcagtatgatcggagattggctacgggttctgtccaaaaagacaaa 1437
Db    940 CTTTGCGGCTGTTCTGAGCATGATTGGAGACTGGCTACGGGTGATATCTAAGAAGACGAA 999

Qy   1438 agaagaggtgggtgaaatcaaggcccatgcggcagagtggaaggccaatgtcacggctga 1497
Db   1000 GGAAGAGGTGGGAGAGTTCAGAGCGCATGCCGCTGAGTGGACAGCCAATGTCACAGCCGA 1059

Qy   1498 gttccgggagacacggcgaaggctcagcgtggagatccacgataagctgcagcgggcggc 1557
Db   1060 GTTCAAGGAAACAAGGAGGCGGCTGAGTGTGGAGATCTATGACAAGTTCCAGCGTGCCAC 1119

Qy   1558 caccat 1563
Db   1120 GTCCGT 1125
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RESULT   8
MMU73488
LOCUS       MMU73488                3580 bp    mRNA    linear   ROD 15-APR-1999
DEFINITION  Mus musculus TREK-1 K+ channel subunit mRNA, complete cds.
ACCESSION   U73488
VERSION     U73488.2  GI:4584798
KEYWORDS    .
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 3580)
  AUTHORS   Fink,M., Duprat,F., Lesage,F., Reyes,R., Romey,G., Heurteaux,C. and
            Lazdunski,M.
  TITLE     Cloning, functional expression and brain localization of a novel
            unconventional outward rectifier K+ channel
  JOURNAL   EMBO J. 15 (24), 6854-6862 (1996)
  MEDLINE   97157476
REFERENCE   2  (bases 1 to 3580)
  AUTHORS   Fink,M., Duprat,F., Lesage,F., Reyes,R., Romey,G., Heurteaux,C. and
            Lazdunski,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-OCT-1996) IPMC, CNRS, 660, route des Lucioles,
            Valbonne 06560, France
REFERENCE   3  (bases 1 to 3580)
  AUTHORS   Fink,M., Duprat,F., Lesage,F., Reyes,R., Romey,G., Heurteaux,C. and
            Lazdunski,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-APR-1999) IPMC, CNRS, 660, route des Lucioles,
            Valbonne 06560, France
  REMARK    Sequence update by submitter
COMMENT     On Apr 15, 1999 this sequence version replaced gi:1794281.
FEATURES             Location/Qualifiers
     source          1. .3580
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /tissue_type="brain"
     CDS             484. .1719
                     /note="pore-forming K+ channel subunit"
                     /codon_start=1
                     /product="TREK-1 K+ channel subunit"
                     /protein_id="AAC53005.2"
                     /db_xref="GI:4584799"
                     /translation="MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKW
                     KTVSTIFLVVVLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDEL
                     IQQIVAAINAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCI
                     IYALLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFG
                     CVLFVALPAVIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGGSDIEYLDFYKPVVWF
                     WILVGLAYFAAVLSMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSV
                     EIYDKFQRATSVKRKLSAELAGNHNQELTPCRRTLSVNHLTSEREVLPPLLKAESIYL
                     NGLTPHCAGEDIAVIENMK"
BASE COUNT      870 a    917 c    913 g    880 t
ORIGIN
```

Query Match 22.7%; Score 469.6; DB 10; Length 3580;
Best Local Similarity 67.5%; Pred. No. 9.4e-98;
Matches 693; Conservative 0; Mismatches 324; Indels 9; Gaps 2;

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Qy    538 gcaaccccggctccggctccgactccaactccgcgcctgtccatttcctcccgagccac 597
Db    504 GGATCCCAAGTCTGCTGCTCAGAACTCCAAACCGAGGCTCTCATTCTCCTCAAAACCCAC 563

Qy    598 agtggtagccaggatggaaggcacctcccaaggggggcttgcagaccgtcatgaagtggaa 657
Db    564 CGTGCTTGCTTCCCGGGTGGAGAGTGACTCGG------CCATTAATGTTATGAAATGGAA 617

Qy    658 gacggtggttgccatctttgtggttgtggtggtctaccttgtcactggcggtcttgtctt 717
Db    618 GACAGTCTCCACGATTTTCCTGGTGGTCGTCCTCTACCTGATCATCGGAGCCGCGGTGTT 677

Qy    718 ccgggcattggagcagccctttgagagcagccagaagaataccatcgccttggagaaggc 777
Db    678 CAAGGCATTGGAGCAGCCTCAGGAGATTTCCCAGAGGACCACCATTGTGATCCAGAAGCA 737

Qy    778 ggaattcctgcgggatcatgtctgtgtgagcccccaggagctggagacgttgatccagca 837
Db    738 GACCTTCATAGCCCAGCATGCCTGCGTCAACTCCACCGAGCTGGACGAACTCATCCAGCA 797

Qy    838 tgctcttgatgctgacaatgcgggagtcagtccaataggaaactcttccaacaacagcag 897
Db    798 AATAGTGGCAGCAATAAACGCAGGGATTATCCCCTTAGGAAACAGCTCCAATCAAGTTAG 857

Qy    898 ccactgggacctcggcagtgccttttttctttgctggaactgtcattacgaccatagggta 957
Db    858 TCACTGGGACCTCGGAAGCTCTTTCTTCTTTGCTGGTACTGTTATCACAACCATAGGATT 917

Qy    958 tgggaatattgctccgagcactgaaggaggcaaaatcttttgtattttatatgccatctt 1017
Db    918 TGGAAACATCTCCCCACGAACTGAAGGTGGAAAAATATTCTGCATCATCTATGCCTTGCT 977
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Qy   1018 tggaattccactctttggtttcttattggctggaattggagaccaacttggaaccatctt 1077
          |||||||| |||||||| ||  || |||||||  |||| || || || ||||| || ||
Db    978 GGGAATTCCCCTCTTTGGCTTTCTACTGGCTGGGGTTGGTGATCAGCTAGGAACTATATT 1037

Qy   1078 tgggaaaagcattgcaagagtggagaaggtctttcgaaaaaagcaagtgagtcagaccaa 1137
          ||| ||| | ||||| | ||||||  |    |||   ||   | | || ||||||||  ||
Db   1038 TGGAAAAGGAATTGCCAAAGTGGAAGACACATTTATTAAGTGGAATGTTAGTCAGACGAA 1097

Qy   1138 gatccgggtcatctcaaccatcctgttcatcttggccggctgcattgtgtttgtgacgat 1197
          ||| ||  |||||||  |||||| | |||||| ||   |||||  |  | |||||| |  |
Db   1098 GATTCGTATCATCTCCACCATCATCTTCATCCTGTTTGGCTGTGTCCTCTTTGTGGCTCT 1157

Qy   1198 ccctgctgtcatctttaagtacatcgagggctggacggccttggagtccatttactttgt 1257
          |||||| ||||| || ||| |||| || |||||||  ||| ||||  | || || |||||
Db   1158 CCCTGCGGTCATATTCAAGCACATAGAAGGCTGGAGCGCCCTGGACGCTATCTATTTTGT 1217

Qy   1258 ggtggtcactctgaccacggtgggctttggtgattttgtggcaggggaaacgctggcat 1317
          |||  |||||||||| ||  | || ||||| || |  |||||||| |||    | | |||
Db   1218 GGTTATCACTCTGACGACCATTGGATTTGGAGACTACGTGGCAGGTGGA---TCAGACAT 1274

Qy   1318 caattatcgggagtggtataagcccctagtgtggttttggatccttgttggccttgccta 1377
            | |||| ||| |  || |||||  | |||||||| |||||||| ||||| || |||||
Db   1275 TGAATATCTGGACTTCTACAAGCCTGTGGTGTGGTTCTGGATCCTCGTTGGGCTGGCCTA 1334

Qy   1378 ctttgcagctgtcctcagtatgatcggagattggctacgggttctgtccaaaaagacaaa 1437
          |||||||||||| || || ||||| || || ||||||||||  | || || |||||  ||
Db   1335 CTTTGCAGCTGTTCTGAGCATGATTGGGGACTGGCTACGGGTGATCTCTAAGAAGACGAA 1394

Qy   1438 agaagaggtgggtgaaatcaaggcccatgcggcagagtggaaggccaatgtcacggctga 1497
          ||||||||||| ||  |||  || ||||| || |||||||  |||||||||||||| ||
Db   1395 GGAAGAGGTGGGAGAGTTCAGAGCGCATGCCGCTGAGTGGACAGCCAATGTCACGGCCGA 1454

Qy   1498 gttccgggagacacggcgaaggctcagcgtggagatccacgataagctgcagcgggcggc 1557
          ||||  ||| ||  || |  |||| |||||||||||| |||| ||| | ||||| ||  |
Db   1455 GTTCAAGGAAACGAGGAGGCGGCTGAGCGTGGAGATCTACGACAAGTTCCAGCGTGCCAC 1514

Qy   1558 caccat 1563
            || |
Db   1515 ATCCGT 1520


RESULT   9
AF129399
LOCUS       AF129399                1236 bp    mRNA    linear   PRI 29-MAR-2001
DEFINITION  Homo sapiens TREK-1 potassium channel (KCNK2) mRNA, complete cds.
ACCESSION   AF129399
VERSION     AF129399.1  GI:5712620
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1236)
  AUTHORS   Patel,A.J., Honore,E., Lesage,F., Fink,M., Romey,G. and
            Lazdunski,M.
  TITLE     Inhalational anesthetics activate two-pore-domain background K+
            channels
  JOURNAL   Nat. Neurosci. 2 (5), 422-426 (1999)
  MEDLINE   99254548
   PUBMED   10321245
REFERENCE   2  (bases 1 to 1236)
  AUTHORS   Patel,A.J., Honore,E., Lesage,F., Fink,M., Romey,G. and
            Lazdunski,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-FEB-1999) IPMC, CNRS, 660 route des lucioles, Sophia
            Antipolis, Valbonne 06560, France
FEATURES             Location/Qualifiers
     source          1. .1236
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     gene            1. .1236
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     CDS             1. .1236
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BASE COUNT      330 a    279 c    299 g    328 t
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  Query Match             22.7%;  Score 468.2;  DB 9;  Length 1236;
  Best Local Similarity   70.0%;  Pred. No. 1.7e-97;
  Matches  645;  Conservative    0;  Mismatches  273;  Indels    3;  Gaps    1;

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Qy    824 acgttgatccagcatgctcttgatgctgacaatgcgggagtcagtccaataggaaactct 883
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Qy    884 tccaacaacagcagccactgggacctcggcagtgccttttttctttgctggaactgtcatt 943
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RESULT  10
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LOCUS       AR156458               1246 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 1 from patent US 6242217.
ACCESSION   AR156458
VERSION     AR156458.1  GI:15125162
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1246)
  AUTHORS   Meadows,H.Jane and Chapman,C.Gerald.
  TITLE     h-TREK1 polypeptides and h-TREK1 polynucleotides
  JOURNAL   Patent: US 6242217-A 1 05-JUN-2001;
FEATURES             Location/Qualifiers
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BASE COUNT      335 a    280 c    302 g    329 t
ORIGIN


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  Best Local Similarity   70.0%;  Pred. No. 1.7e-97;
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RESULT  11
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LOCUS       AX003047               1246 bp    DNA     linear   PAT 24-AUG-2000
DEFINITION  Sequence 1 from Patent WO9937762.
ACCESSION   AX003047
VERSION     AX003047.1  GI:9926934
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1246)
  AUTHORS   Chapman,C.G. and Meadows,H.J.
  TITLE     Trek-1 like two pore potassium channel
  JOURNAL   Patent: WO 9937762-A 1 29-JUL-1999;
            SMITHKLINE BEECHAM PLC (GB)
FEATURES             Location/Qualifiers
     source          1. .1246
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                     /db_xref="taxon:9606"
BASE COUNT      335 a    280 c    302 g    329 t
ORIGIN


  Query Match             22.7%;  Score 468.2;  DB 6;  Length 1246;
  Best Local Similarity   70.0%;  Pred. No. 1.7e-97;
  Matches  645;  Conservative    0;  Mismatches  273;  Indels    3;  Gaps    1;

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Db    669 CTCTTTGTGGCTCTGCCTGCGATCATATTCAAACACATAGAAGGCTGGAGTGCCCTGGAC 728

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RESULT  12
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DEFINITION  Sequence 1 from Patent WO0072863.
ACCESSION   AX054800
VERSION     AX054800.1  GI:12228256
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1246)
  AUTHORS   Hervieu,G.J., Meadows,H.J. and Randall,A.D.
  TITLE     Uses of h-trek-1 polypeptides and polynucleotides encoding them
  JOURNAL   Patent: WO 0072863-A 1 07-DEC-2000;
            SMITHKLINE BEECHAM PLC (GB)
FEATURES             Location/Qualifiers
     source          1. .1246
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BASE COUNT      335 a    280 c    302 g    329 t
ORIGIN


  Query Match             22.7%;  Score 468.2;  DB 6;  Length 1246;
  Best Local Similarity   70.0%;  Pred. No. 1.7e-97;
  Matches  645;  Conservative    0;  Mismatches  273;  Indels    3;  Gaps    1;

Qy    644 gtcatgaagtggaagacggtggttgccatctttgtggttgtggtggtctaccttgtcact 703
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Qy   1544 ctgcagcgggcggccaccatc 1564
Db   1026 TTCCAGCGGGCCACCTCCATC 1046
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RESULT 13
AF171068
LOCUS       AF171068               1252 bp    mRNA    linear   PRI 13-JUN-2001
DEFINITION  Homo sapiens two-pore domain potassium channel TREK-1 (TREK-1)
            mRNA, complete cds.
ACCESSION   AF171068
VERSION     AF171068.1  GI:9622334
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1252)
  AUTHORS   Meadows,H.J., Benham,C.D., Cairns,W., Gloger,I.S., Jennings,C.,
            Medhurst,A.D., Murdock,P. and Chapman,C.G.
  TITLE     Cloning, localisation and functional expression of the human
            orthologue of the TREK-1 potassium channel
  JOURNAL   Pflugers Arch. 439 (6), 714-722 (2000)
  MEDLINE   20244931
   PUBMED   10784345
REFERENCE   2  (bases 1 to 1252)
  AUTHORS   Chapman,C.G., Gloger,I.S. and Meadows,H.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-JUL-1999) Biotechnology & Genetics, SmithKline
            Beecham Pharmaceuticals, New Frontiers Science Park (North), Third
            Avenue, Harlow, Essex CM19 5AW, UK
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ORIGIN
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Best Local Similarity 70.0%; Pred. No. 1.7e-97;
Matches 645; Conservative 0; Mismatches 273; Indels 3; Gaps 1;

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SOURCE      Mus sp.
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REFERENCE   1  (bases 1 to 1993)
  AUTHORS   Fink,M., Honore,E., Duprat,F., Lesage,F. and Lazdunski,M.
  TITLE     Novel mechanically sensitive mammal potassium channel family
            activated by polyunsaturated fatty acids and their use particularly
            for screening medicines
  JOURNAL   Patent: WO 9945108-A 2 10-SEP-1999;
            FINK MICHEL (FR); HONORE ERIC (FR); DUPRAT FABRICE (FR); LESAGE
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ACCESSION   AR156460
VERSION     AR156460.1  GI:15125164
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            Unclassified.
REFERENCE   1  (bases 1 to 1994)
  AUTHORS   Meadows,H.Jane and Chapman,C.Gerald.
  TITLE     h-TREK1 polypeptides and h-TREK1 polynucleotides
  JOURNAL   Patent: US 6242217-A 5 05-JUN-2001;
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: September 21, 2002, 06:42:59 ; Search time 333.79 Seconds
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Perfect score: 2065
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Scoring table: IDENTITY_NUC
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Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	721.2	34.9	779	22	AAH98807	Human EST-derived
	3	619.8	30.0	1671	23	AAS72492	DNA encoding novel
	4	469.6	22.7	3580	21	AAD17497	Murine TREK-1 pota
	5	468.2	22.7	1236	21	AAD17496	Human TREK-1 potas
	6	468.2	22.7	1246	20	AAZ00039	h-TREK1 polynucleo
	7	468.2	22.7	1246	22	AAC90412	Human TREK coding
	8	468.2	22.7	3300	20	AAZ11915	Human potassium ch
	9	468	22.7	1993	20	AAZ10607	cDNA encoding a me
	10	468	22.7	1994	20	AAZ00040	Mouse h-TREK1 poly
	11	458.6	22.2	2130	22	AAS12169	Human potassium io
	12	458.6	22.2	2130	22	AAS12181	Human potassium io
	13	457	22.1	2130	22	AAS12182	Human potassium io
	14	457	22.1	2130	22	AAS12184	Human potassium io
	15	455.4	22.1	2130	22	AAS12183	Human potassium io
c	16	405.4	19.6	458	23	AAS66917	DNA encoding novel
	17	280.8	13.6	3945	22	AAS11984	Human cDNA encodin
	18	279.2	13.5	1218	21	AAA27106	Human h-TRAAK cDNA
	19	279.2	13.5	1257	24	AAH99922	Nucleotide sequenc
	20	279.2	13.5	1408	24	AAH99921	Nucleotide sequenc
	21	279.2	13.5	3996	22	AAS08652	Human cDNA encodin
	22	276.8	13.4	1182	21	AAA27105	Human h-TRAAK cDNA
	23	276.8	13.4	1182	22	AAH78636	Human mechanically
	24	250.8	12.1	1794	20	AAZ10606	cDNA encoding a me
c	25	190.4	9.2	557	22	ABA61503	Human foetal liver
c	26	190.4	9.2	557	22	AAK09803	Human brain expres
c	27	190.4	9.2	557	22	AAK35697	Human bone marrow
c	28	190.4	9.2	557	22	AAI41412	Probe #10098 used
	29	188.8	9.1	270	22	ABA75754	Human foetal liver
	30	188.8	9.1	270	22	AAK24387	Human brain expres
	31	188.8	9.1	270	22	AAI56375	Probe #25061 used
	32	188.8	9.1	547	22	ABA63312	Human foetal liver
	33	188.8	9.1	547	22	AAK11797	Human brain expres
	34	188.8	9.1	547	22	AAI43395	Probe #12081 used
c	35	187	9.1	187	22	ABA74001	Human foetal liver
c	36	187	9.1	187	22	AAK22454	Human brain expres
c	37	187	9.1	187	22	AAK48622	Human bone marrow
c	38	187	9.1	187	22	AAI54450	Probe #23136 used
	39	181	8.8	321	20	AAZ00041	Partial h-TREK1 po
	40	164.4	8.0	723	23	AAS71420	DNA encoding novel
c	41	142.8	6.9	885	23	AAS66919	DNA encoding novel
	42	140.4	6.8	3768	21	AAA15953	Human protein clon
	43	140.2	6.8	1497	21	AAA15943	Human protein clon
	44	140.2	6.8	1498	21	AAA37771	Human TWIK-2 codin
	45	140.2	6.8	1839	23	AAS90940	DNA encoding novel

ALIGNMENTS

RESULT 1
AAS66918
ID AAS66918 standard; cDNA; 1152 BP.
XX
AC AAS66918;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #2722.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG02731.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in

```
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity  -
XX
PS   Claim 1; SEQ ID No 2722; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human
CC   diagnostic coding sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1152 BP; 312 A; 295 C; 318 G; 227 T; 0 other;


  Query Match             46.0%;  Score 949.8;  DB 23;  Length 1152;
  Best Local Similarity   99.8%;  Pred. No. 1.8e-233;
  Matches  951;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy   1113 gaaaaaagcaagtgagtcagaccaagatccgggtcatctcaaccatcctgttcatcttgg 1172
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    200 ggaaaaagcaagtgagtcagaccaagatccgggtcatctcaaccatcctgttcatcttgg 259

Qy   1173 ccggctgcattgtgtttgtgacgatccctgctgtcatctttaagtacatcgagggctgga 1232
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    260 ccggctgcattgtgtttgtgacgatccctgctgtcatctttaagtacatcgagggctgga 319

Qy   1233 cggccttggagtccatttactttgtggtggtcactctgaccacggtgggctttggtgatt 1292
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    320 cggccttggagtccatttactttgtggtggtcactctgaccacggtgggctttggtgatt 379

Qy   1293 ttgtggcaggggaaacgctggcatcaattatcgggagtggtataagcccctagtgtggt 1352
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    380 ttgtggcaggggaaacgctggcatcaattatcgggagtggtataagcccctagtgtggt 439

Qy   1353 tttggatccttgttggccttgcctactttgcagctgtcctcagtatgatcggagattggc 1412
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    440 tttggatccttgttggccttgcctactttgcagctgtcctcagtatgatcggagattggc 499

Qy   1413 tacgggttctgtccaaaaagacaaaagaagaggtgggtgaaatcaaggcccatgcggcag 1472
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    500 tacgggttctgtccaaaaagacaaaagaagaggtgggtgaaatcaaggcccatgcggcag 559

Qy   1473 agtggaaggccaatgtcacggctgagttccgggagacacggcgaaggctcagcgtggaga 1532
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    560 agtggaaggccaatgtcacggctgagttccgggagacacggcgaaggctcagcgtggaga 619

Qy   1533 tccacgataagctgcagcgggcggccaccatccgcagcatggagcgccggcggctgggcc 1592
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    620 tccacgataagctgcagcgggcggccaccatccgcagcatggagcgccggcggctgggcc 679

Qy   1593 tggaccagcgggcccactcactggacatgctgtcccccgagaagcgctctgtctttgctg 1652
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    680 tggaccagcgggcccactcactggacatgctgtcccccgagaagcgctctgtctttgctg 739

Qy   1653 ccctggacaccggccgcttcaaggcctcatcccaggagagcatcaacaaccggcccaaca 1712
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db    740 ccctggacaccggccgcttcaaggcctcatcccaggagagcatcaacaaccggcccaaca 799

Qy   1713 acctgcgcctgaaggggccggagcagctgaacaagcatgggcagggtgcgtccgaggaca 1772
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    800 acctgcgcctgaaggggccggagcagctgaacaagcatgggcagggtgcgtccgaggaca 859

Qy   1773 acatcatcaacaagttcgggtccacctccagactcaccaagaggaaaaacaaggacctca 1832
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    860 acatcatcaacaagttcgggtccacctccagactcaccaagaggaaaaacaaggacctca 919

Qy   1833 aaaagaccttgcccgaggacgttcagaaaatctacaagaccttccggaattactccctgg 1892
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    920 aaaagaccttgcccgaggacgttcagaaaatctacaagaccttccggaattactccctgg 979

Qy   1893 acgaggagaagaaagaggaggaaacggaaaagatgtgtaactcagacaactccagcacag 1952
           |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    980 acgaggagaagaaagaggaggagacggaaaagatgtgtaactcagacaactccagcacag 1039

Qy   1953 ccatgctgacggactgtatccagcagcacgctgagttggagaacggaatgatacccacgg 2012
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1040 ccatgctgacggactgtatccagcagcacgctgagttggagaacggaatgatacccacgg 1099

Qy   2013 acaccaaagaccgggagccggagaacaactcattacttgaagacagaaactaa 2065
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1100 acaccaaagaccgggagccggagaacaactcattacttgaagacagaaactaa 1152


RESULT   2
AAH98807
ID   AAH98807 standard; cDNA; 779 BP.
XX
AC   AAH98807;
XX
DT   12-OCT-2001  (first entry)
XX
DE   Human EST-derived coding sequence SEQ ID NO: 664.
XX
KW   Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW   tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW   diagnostics; forensic test; gene mapping; genetic disorder;
KW   biodiversity; gene therapy; nutrition; ss.
XX
OS   Homo sapiens.
XX
PN   WO200154477-A2.
XX
PD   02-AUG-2001.
XX
PF   25-JAN-2001; 2001WO-US02687.
XX
PR   25-JAN-2000; 2000US-0491404.
PR   17-JUL-2000; 2000US-0617746.
PR   03-AUG-2000; 2000US-0631451.
PR   15-SEP-2000; 2000US-0663870.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Zhou P,  Qian XB,  Wang Z,  Chen R,  Asundi V;
PI   Cao Y,  Drmanac RA,  Zhang J,  Werhman T;
XX
DR   WPI; 2001-476164/51.
DR   P-PSDB; AAM24148.
XX
PT   Isolated polypeptide for treatment of diseases, diagnostics, raising
PT   antibodies and research use -
XX
PS   Claim 1; Page 621; 1275pp; English.
XX
CC   The present invention provides the protein and coding sequences of novel
CC   proteins from a variety of organisms, including human, dog, cat, horse,
CC   cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC   urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC   from the organism of interest. They can be used in diagnostics,
```

```
CC   forensics, gene mapping, identification of mutations, to assess
CC   biodiversity and for nutritional purposes. The present sequence is a cDNA
CC   of the invention.
XX
SQ   Sequence 779 BP; 170 A; 175 C; 221 G; 213 T; 0 other;


  Query Match             34.9%;  Score 721.2;  DB 22;  Length 779;
  Best Local Similarity   97.0%;  Pred. No. 6.7e-175;
  Matches  735;  Conservative    0;  Mismatches   23;  Indels    0;  Gaps    0;

Qy     597 cagtggtagccaggatggaaggcacctcccaaggggcttgcagaccgtcatgaagtgga 656
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8 cagtggtagccaggatggaaggcacctcccaaggggcttgcagaccgtcatgaagtgga 67

Qy     657 agacggtggttgccatctttgtggttgtggtggtctaccttgtcactggcggtcttgtct 716
           |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      68 agacgggggttgccatctttgtggttgtggtggtctaccttgtcactggcggtcttgtct 127

Qy     717 tccgggcattggagcagccctttgagagcagccagaagaataccatcgccttggagaaagg 776
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     128 tccgggcattggagcagccctttgagagcagccagaagaataccatcgccttggagaaagg 187

Qy     777 cggaattcctgcgggatcatgtctgtgtgagcccccaggagctggagacgttgatccagc 836
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     188 cggaattcctgcgggatcatgtctgtgtgagcccccaggagctggagacgttgatccagc 247

Qy     837 atgctcttgatgctgacaatgcgggagtcagtccaataggaaactcttccaacaacagca 896
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     248 atgctcttgatgctgacaatgcgggagtcagtccaataggaaactcttccaacaacagca 307

Qy     897 gccactgggacctcggcagtgccttttttctttgctggaactgtcattacgaccatagggt 956
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     308 gccactgggacctcggcagtgccttttttctttgctggaactgtcattacgaccatagggt 367

Qy     957 atgggaatattgctccgagcactgaaggaggcaaaatcttttgtattttatatgccatct 1016
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     368 atgggaatattgctccgagcactgaaggaggcaaaatcttttgtattttatatgccatct 427

Qy    1017 ttggaattccactctttggtttcttattggctggaattggagaccaacttggaaccatct 1076
           ||||| |||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db     428 ttggatttccactctttggtttcttattggctggaattgaagaccaacttggaaccatct 487

Qy    1077 ttgggaaaagcattgcaagagtggagaaggtctttcgaaaaaagcaagtgagtcagacca 1136
           |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db     488 ttgggaaaagcattgcaagagtggagaaggtctttttgaaaaaagcaagtgagtcagacca 547

Qy    1137 agatccgggtcatctcaaccatcctgttcatcttggccggctgcattgtgtttgtgacga 1196
           |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     548 agattcgggtcatctcaaccatcctgttcatcttggccggctgcattgtgtttgtgacga 607

Qy    1197 tccctgctgtcatctttaagtacatcgagggctggacggccttggagtccatttactttg 1256
           |||||||||||||| ||||||| |||||||||||||||| ||||||||||||||||||||
Db     608 tccctgctgtcatctataagtacttcgagggctggacggctttggagtccatttactttg 667

Qy    1257 tggtggtcactctgaccacggtgggctttggtgattttgtggcaggggaaaacgctggca 1316
           |||||||||||| | |||||||||||||||||||||||||||||||  || ||||||||
Db     668 tggtggtcactccgcccacggtgggctttggtgattttgtggcagggaaaaccgctggca 727

Qy    1317 tcaattatcgggagtggtataagcccctagtgtggttt 1354
           |||||||||| |||  ||||  ||||   ||| ||| |
Db     728 tcaattatcgagaggtgtattcgcccgctgtggggtct 765


RESULT   3
AAS72492
ID   AAS72492 standard; cDNA; 1671 BP.
XX
AC   AAS72492;
XX
DT   13-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #8296.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   P-PSDB; ABG08305.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity  -
XX
PS   Claim 1; SEQ ID No 8296; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human
CC   diagnostic coding sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1671 BP; 540 A; 375 C; 462 G; 294 T; 0 other;


  Query Match             30.0%;  Score 619.8;  DB 23;  Length 1671;
  Best Local Similarity   99.7%;  Pred. No. 9.6e-149;
  Matches  621;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    1443 aggtgggtgaaatcaaggcccatgcggcagagtggaaggccaatgtcacggctgagttcc 1502
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Db    1049 acgtgggtgaaatcaaggcccatgcggcagagtggaaggccaatgtcacggctgagttcc 1108

Qy    1503 gggagacacggcgaaggctcagcgtggagatccacgataagctgcagcgggcggccacca 1562
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Db    1109 gggagacacggcgaaggctcagcgtggagatccacgataagctgcagcgggcggccacca 1168

Qy    1563 tccgcagcatggagcgccggcggctgggcctggaccagcgggcccactcactggacatgc 1622
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1169 tccgcagcatggagcgccggcggctgggcctggaccagcgggcccactcactggacatgc 1228

Qy    1623 tgtcccccgagaagcgctctgtctttgctgccctggacaccggccgcttcaaggcctcat 1682
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1229 tgtcccccgagaagcgctctgtctttgctgccctggacaccggccgcttcaaggcctcat 1288
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Qy   1683 cccaggagagcatcaacaaccggcccaacaacctgcgcctgaaggggccggagcagctga 1742
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1289 cccaggagagcatcaacaaccggcccaacaacctgcgcctgaaggggccggagcagctga 1348

Qy   1743 acaagcatgggcagggtgcgtccgaggacaacatcatcaacaagttcgggtccacctcca 1802
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1349 acaagcatgggcagggtgcgtccgaggacaacatcatcaacaagttcgggtccacctcca 1408

Qy   1803 gactcaccaagaggaaaaacaaggacctcaaaaagaccttgcccgaggacgttcagaaaa 1862
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1409 gactcaccaagaggaaaaacaaggacctcaaaaagaccttgcccgaggacgttcagaaaa 1468

Qy   1863 tctacaagaccttccggaattactccctggacgaggagaagaaagaggaggaaacggaaa 1922
          |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db   1469 tctacaagaccttccggaattactccctggacgaggagaagaaagaggaggagacggaaa 1528

Qy   1923 agatgtgtaactcagacaactccagcacagccatgctgacggactgtatccagcagcacg 1982
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1529 agatgtgtaactcagacaactccagcacagccatgctgacggactgtatccagcagcacg 1588

Qy   1983 ctgagttggagaacggaatgatacccacggacaccaaagaccgggagccggagaacaact 2042
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1589 ctgagttggagaacggaatgatacccacggacaccaaagaccgggagccggagaacaact 1648

Qy   2043 cattacttgaagacagaaactaa 2065
          |||||||||||||||||||||||
Db   1649 cattacttgaagacagaaactaa 1671
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RESULT 4
AAD17497
ID AAD17497 standard; DNA; 3580 BP.
XX
AC AAD17497;
XX
DT 10-DEC-2001 (first entry)
XX
DE Murine TREK-1 potassium channel protein DNA.
XX
KW Murine; potassium channel protein; TREK-1; anaesthetic; analgesia;
KW amnesia; ds.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT CDS 484..1719
FT /*tag= a
FT /product= "Murine TREK-1 potassium channel protein"
XX
PN WO200047738-A2.
XX
PD 17-AUG-2000.
XX
PF 11-FEB-2000; 2000WO-IB00226.
XX
PR 12-FEB-1999; 99US-0119727.
PR 11-FEB-2000; 2000US-0503089.
XX
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Lazdunski M, Honore E, Lesage F, Romey G, Patel AJ;
XX
DR WPI; 2000-549146/50.
DR P-PSDB; AAE10342.
XX
PT Novel nucleic acid encoding a TREK-1 potassium channel protein for
PT transfecting cells to be used to identify compounds with anesthetic
PT properties -
XX
PS Claim 7; Page 29-31; 39pp; English.
XX
CC The invention relates to human and mouse TREK-1 potassium channel
CC proteins and their corresponding DNA molecules. TREK-1 nucleic acid is
CC useful for transfecting cells to induce expression of the TREK-1
CC potassium channel protein. These cells are then used in assays to
CC identify compounds which have anaesthetic properties, producing a safe,
CC reversible state of unconsciousness with concurrent amnesia and analgesia
CC in a mammal upon inhalation. The present DNA sequence encodes murine
CC TREK-1 potassium channel protein.
XX
SQ Sequence 3580 BP; 870 A; 917 C; 913 G; 880 T; 0 other;

```
  Query Match             22.7%;  Score 469.6;  DB 21;  Length 3580;
  Best Local Similarity   67.5%;  Pred. No. 4.5e-110;
  Matches  693;  Conservative    0;  Mismatches  324;  Indels    9;  Gaps    2;

Qy    538 gcaacccccggctccggctccgactccaactccgcgcctgtccatttcctcccgagccac 597
          | | |||  | || | |||| ||   | |  ||| | || ||  | |||||   | ||||
Db    504 ggatcccaagtctgctgctcagaactccaaaccgaggctctcattctcctcaaaacccac 563

Qy    598 agtggtagccaggatggaaggcacctcccaaggggcttgcagaccgtcatgaagtggaa 657
           ||| | ||      || |  |    |  |           |  || ||||| |||||
Db    564 cgtgcttgcttcccgggtggagagtgactcgg------ccattaatgttatgaaatggaa 617

Qy    658 gacggtggttgccatctttgtggttgtggtggtctaccttgtcactggcggtcttgtctt 717
          ||| ||     | || ||  |||| || ||  |||||||  |||  || |     || ||
Db    618 gacagtctccacgattttcctggtggtcgtcctctacctgatcatcggagccgcggtgtt 677

Qy    718 ccgggcattggagcagccctttgagagcagccagaagaataccatcgccttggagaaggc 777
          |  ||||||||||||||    ||||   ||||| ||  ||||| |   |  |||||
Db    678 caaggcattggagcagcctcaggagatttcccagaggaccaccattgtgatccagaagca 737

Qy    778 ggaattcctgcgggatcatgtctgtgtgagcccccaggagctggagacgttgatccagca 837
          |   ||| |     | |||| ||| || | | ||   ||||||||     | ||||||||
Db    738 gaccttcatagcccagcatgcctgcgtcaactccaccgagctggacgaactcatccagca 797

Qy    838 tgctcttgatgctgacaatgcgggagtcagtccaataggaaactcttccaacaacagcag 897
            | |  ||    || || ||  | |  ||  ||||||||   |||||  |    ||
Db    798 aatagtggcagcaataaacgcagggattatccccttaggaaacagctccaatcaagttag 857

Qy    898 ccactgggacctcggcagtgccttttttctttgctggaactgtcattacgaccatagggta 957
          ||||||||||||| ||  | || ||||||||||| ||||| || || |||||||| |
Db    858 tcactgggacctcggaagctctttcttctttgctggtactgttatcacaaccataggatt 917

Qy    958 tgggaatattgctccgagcactgaaggaggcaaaatcttttgtattttatatgccatctt 1017
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Db    918 tggaaacatctccccacgaactgaaggtggaaaaatattctgcatcatctatgccttgct 977

Qy   1018 tggaattccactctttggtttcttattggctggaattggagaccaacttggaaccatctt 1077
          ||||||||  ||||||||  ||  || |||||||  |||| || || || ||||| || ||
Db    978 gggaattcccctctttggctttctactggctggggttggtgatcagctaggaactatatt 1037

Qy   1078 tgggaaaagcattgcaagagtggagaaggtctttcgaaaaaagcaagtgagtcagaccaa 1137
          ||| ||| | ||||| | ||||||  |    |||   ||   | | || |||||||| ||
Db   1038 tggaaaaggaattgccaaagtggaagacacatttattaagtggaatgttagtcagacgaa 1097

Qy   1138 gatccgggtcatctcaaccatcctgttcatcttggccggctgcattgtgtttgtgacgat 1197
          ||| ||  ||||||| ||||||| | ||||||  ||   |||||  |  | ||||||  |  |
Db   1098 gattcgtatcatctccaccatcatcttcatcctgtttggctgtgtcctctttgtggctct 1157

Qy   1198 ccctgctgtcatctttaagtacatcgagggctggacggccttggagtccatttacttttgt 1257
          |||||| ||||| || ||| |||| || |||||||  ||| ||||  | || || |||||
Db   1158 ccctgcggtcatattcaagcacatagaaggctggagcgccctggacgctatctattttgt 1217

Qy   1258 ggtggtcactctgaccacggtgggctttggtgattttgtggcaggggaaacgctggcat 1317
          |||  ||||||||||| ||  | || ||||| || |  ||||||||  |||    | | |||
Db   1218 ggttatcactctgacgaccattggatttggagactacgtggcaggtgga---tcagacat 1274

Qy   1318 caattatcgggagtggtataagcccctagtgtggttttggatccttgttggccttgccta 1377
            | |||| ||| |  || |||||  | ||||||||  |||||||| ||||| || |||||
Db   1275 tgaatatctggacttctacaagcctgtggtgtggttctggatcctcgttgggctggccta 1334

Qy   1378 ctttgcagctgtcctcagtatgatcggagattggctacgggttctgtccaaaaagacaaa 1437
          |||||||||||| || || ||||| || || ||||||||||  | || || ||||| ||
```

```
Db   1335 ctttgcagctgttctgagcatgattggggactggctacgggtgatctctaagaagacgaa 1394

Qy   1438 agaagaggtgggtgaaatcaaggcccatgcggcagagtggaaggccaatgtcacggctga 1497

Db   1395 ggaagaggtgggagagttcagagcgcatgccgctgagtggacagccaatgtcacggccga 1454

Qy   1498 gttccgggagacacggcgaaggctcagcgtggagatccacgataagctgcagcgggcggc 1557

Db   1455 gttcaaggaaacgaggaggcggctgagcgtggagatctacgacaagttccagcgtgccac 1514

Qy   1558 caccat 1563

Db   1515 atccgt 1520


RESULT   5
AAD17496
ID   AAD17496 standard; DNA; 1236 BP.
XX
AC   AAD17496;
XX
DT   10-DEC-2001  (first entry)
XX
DE   Human TREK-1 potassium channel protein DNA.
XX
KW   Human; potassium channel protein; TREK-1; anaesthetic; analgesia;
KW   amnesia; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1236
FT                   /*tag=  a
FT                   /product= "Human TREK-1 potassium channel protein"
XX
PN   WO200047738-A2.
XX
PD   17-AUG-2000.
XX
PF   11-FEB-2000; 2000WO-IB00226.
XX
PR   12-FEB-1999;   99US-0119727.
PR   11-FEB-2000; 2000US-0503089.
XX
PA   (CNRS ) CNRS CENT NAT RECH SCI.
XX
PI   Lazdunski M,  Honore E,  Lesage F,  Romey G,  Patel AJ;
XX
DR   WPI; 2000-549146/50.
DR   P-PSDB; AAE10341.
XX
PT   Novel nucleic acid encoding a TREK-1 potassium channel protein for
PT   transfecting cells to be used to identify compounds with anesthetic
PT   properties -
XX
PS   Claim 1; Page 26-28; 39pp; English.
XX
CC   The invention relates to human and mouse TREK-1 potassium channel
CC   proteins and their corresponding DNA molecules. TREK-1 nucleic acid is
CC   useful for transfecting cells to induce expression of the TREK-1
CC   potassium channel protein. These cells are then used in assays to
CC   identify compounds which have anaesthetic properties, producing a safe,
CC   reversible state of unconsciousness with concurrent amnesia and analgesia
CC   in a mammal upon inhalation. The present DNA sequence encodes human
CC   TREK-1 potassium channel protein.
XX
SQ   Sequence 1236 BP; 330 A; 279 C; 299 G; 328 T; 0 other;


  Query Match             22.7%;  Score 468.2;  DB 21;  Length 1236;
  Best Local Similarity   70.0%;  Pred. No. 6.5e-110;
  Matches  645;  Conservative    0;  Mismatches  273;  Indels    3;  Gaps    1;

Qy    644 gtcatgaagtggaagacggtggttgccatctttgtggttgtggtggtctaccttgtcact 703

Db    121 gttatgaaatggaagacggtctccacgatattcctggtggttgtcctctatctgatcatc 180

Qy    704 ggcggtcttgtcttccgggcattggagcagccctttgagagcagccagaagaataccatc 763

Db    181 ggagccaccgtgttcaaagcattggagcagcctcatgagatttcacagaggaccaccatt 240

Qy    764 gccttggagaaggcggaattcctgcgggatcatgtctgtgtgagcccccaggagctggag 823

Db    241 gtgatccagaagcaaacattcatatcccaacattcctgtgtcaattcgacggagctggat 300

Qy    824 acgttgatccagcatgctcttgatgctgacaatgcgggagtcagtccaataggaaactct 883

Db    301 gaactcattcagcaaatagtggcagcaataaatgcagggattataccgttaggaaacacc 360

Qy    884 tccaacaacagcagccactgggacctcggcagtgccttttttctttgctggaactgtcatt 943

Db    361 tccaatcaaatcagtcactgggatttgggaagttccttcttctttgctggcactgttatt 420

Qy    944 acgaccatagggtatgggaatattgctccgagcactgaaggaggcaaaatcttttgtatt 1003

Db    421 acaaccataggatttggaaacatctcaccacgcacagaaggcggcaaaatattctgtatc 480

Qy   1004 ttatatgccatctttggaattccactctttggtttcttattggctggaattggagaccaa 1063

Db    481 atctatgccttactgggaattcccctctttggttttctcttggctggagttggagatcag 540

Qy   1064 cttggaaccatctttgggaaaagcattgcaagagtggagaaggtctttcgaaaaaagcaa 1123

Db    541 ctaggcaccatatttggaaaaggaattgccaaagtggaagatacgtttattaagtggaat 600

Qy   1124 gtgagtcagaccaagatccgggtcatctcaaccatcctgttcatcttggccggctgcatt 1183

Db    601 gttagtcagaccaagattcgcatcatctcaacaatcatatttatactatttggctgtgta 660

Qy   1184 gtgtttgtgacgatccctgctgtcatctttaagtacatcgagggctggacggccttggag 1243

Db    661 ctctttgtggctctgcctgcgatcatattcaaacacatagaaggctggagtgccctggac 720

Qy   1244 tccatttacttttgtggtggtcactctgaccacggtgggctttggtgattttgtggcaggg 1303

Db    721 gccatttattttgtggttatcactctaacaactattggatttggtgactacgttgcaggt 780

Qy   1304 ggaaacgctggcatcaattatcgggagtggtataagcccctagtgtggttttggatcctt 1363

Db    781 ggatccgat---attgaatatctggacttctataagcctgtcgtgtggttctggatcctt 837

Qy   1364 gttggccttgcctactttgcagctgtcctcagtatgatcggagattggctacgggttctg 1423

Db    838 gtagggcttgcttactttgctgctgtcctgagcatgattggagattggctccgagtgata 897

Qy   1424 tccaaaaagacaaaagaagaggtgggtgaaatcaaggcccatgcggcagagtggaaggcc 1483

Db    898 tctaaaaagacaaaagaagaggtgggagagttcagagcacacgctgctgagtggacagcc 957

Qy   1484 aatgtcacggctgagttccgggagacacggcgaaggctcagcgtggagatccacgataag 1543

Db    958 aacgtcacagccgaattcaaagaaaccaggaggcgactgagtgtggagatttatgacaag 1017

Qy   1544 ctgcagcgggcggccaccatc 1564

Db   1018 ttccagcgggccacctccatc 1038


RESULT   6
AAZ00039
ID   AAZ00039 standard; DNA; 1246 BP.
XX
AC   AAZ00039;
XX
DT   12-OCT-1999  (first entry)
XX
```

```
DE   h-TREK1 polynucleotide.
XX
KW   h-TREK1; two pore potassium channel; inflammatory disease;
KW   chromosome 1q32; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             9..1244
FT                   /*tag= a
FT                   /product= "h-TREK1"
XX
PN   WO9937762-A1.
XX
PD   29-JUL-1999.
XX
PF   02-DEC-1998;   98WO-EP07805.
XX
PR   09-OCT-1998;   98GB-0022135.
PR   27-JAN-1998;   98EP-0300570.
XX
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Chapman CG,  Meadows HJ;
XX
DR   WPI; 1999-469126/39.
DR   P-PSDB; AAY28496.
XX
PT   New two pore potassium channel used for, e.g.  treatment of cancer,
PT   pulmonary, cardiovascular and inflammatory diseases
XX
PS   Claim 9; Page 24; 44pp; English.
XX
CC   This sequence is the h-TREK1 polynucleotide, encoding the h-TREK1
CC   polypeptide AAY28496. h-TREK1 is a two pore potassium channel, and the
CC   gene maps to human chromosome 1q32, between the markers D1S237 and
CC   WI5105. The polynucleotide sequence of h-TREK1 can be used to diagnose a
CC   disease or susceptibility to a disease related to expression or activity
CC   of h-TREK-1 polypeptides. The methods of diagnosis may be used in the
CC   treatment of diseases including cancer, pulmonary, cardiovascular, and
CC   inflammatory diseases, pain, psychiatric disorders including depression
CC   and schizophrenia, neurodegenerative diseases including Alzheimer's,
CC   stroke, and head trauma and neurological disorders including migraine.
XX
SQ   Sequence 1246 BP; 335 A; 280 C; 302 G; 329 T; 0 other;

  Query Match            22.7%;  Score 468.2;  DB 20;  Length 1246;
  Best Local Similarity  70.0%;  Pred. No. 6.5e-110;
  Matches  645;  Conservative    0;  Mismatches  273;  Indels    3;  Gaps    1;

Qy     644 gtcatgaagtggaagacggtggttgccatctttgtggttgtggtggtctaccttgtcact 703
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Db     129 gttatgaaatggaagacggtctccacgatattcctggtggttgtcctctatctgatcatc 188

Qy     704 ggcggtcttgtcttccgggcattggagcagccctttgagagcagccagaagaataccatc 763
           || |     || |||   ||||||||||||||   |||||     |||| ||  |||||
Db     189 ggagccaccgtgttcaaagcattggagcagcctcatgagatttcacagaggaccaccatt 248

Qy     764 gccttggagaaggcggaattcctgcgggatcatgtctgtgtgagcccccaggagctggag 823
           |   |  |||||     |||| |     | |||  |||||| |   |   |||||||||
Db     249 gtgatccagaagcaaacattcatatcccaacattcctgtgtcaattcgacggagctggat 308

Qy     824 acgttgatccagcatgctcttgatgctgacaatgcgggagtcagtccaataggaaactct 883
           | || |||||     | |  ||    ||||| ||  | |  ||  |||||||||
Db     309 gaactcattcagcaaatagtggcagcaataaatgcagggattataccgttaggaaacacc 368

Qy     884 tccaacaacagcagccactgggacctcggcagtgccttttttctttgctggaactgtcatt 943
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Db     369 tccaatcaaatcagtcactgggatttgggaagttccttcttctttgctggcactgttatt 428

Qy     944 acgaccatagggtatgggaatattgctccgagcactgaaggaggcaaaatcttttgtatt 1003
           || |||||||| | ||| || ||  | ||  |||| ||||| |||||||| || |||||
               * *     '

Db     429 acaaccataggatttggaaacatctcaccacgcacagaaggcggcaaaatattctgtatc 488

Qy    1004 ttatatgccatctttggaattccactctttggtttcttattggctggaattggagaccaa 1063
           | |||||| |  | |||||||| ||||||||||  | |||||||| ||||||| ||
Db     489 atctatgccttactgggaattcccctctttggttttctcttggctggagttggagatcag 548

Qy    1064 cttggaaccatctttgggaaaagcattgcaagagtggagaaggtctttcgaaaaaagcaa 1123
           || || ||||| ||||| ||| | ||||| | ||||||  |    |||  ||   | |
Db     549 ctaggcaccatatttggaaaaggaattgccaaagtggaagatacgtttattaagtggaat 608

Qy    1124 gtgagtcagaccaagatccgggtcatctcaaccatcctgttcatcttggccggctgcatt 1183
           || |||||||||||||| ||  |||||||||| ||| | || ||  |    |||||  |
Db     609 gttagtcagaccaagattcgcatcatctcaacaatcatatttatactatttggctgtgta 668

Qy    1184 gtgtttgtgacgatccctgctgtcatctttaagtacatcgagggctggacggccttggag 1243
           | |||||| |  | |||||  |||| || ||  |||| || |||||||  ||| ||||
Db     669 ctctttgtggctctgcctgcgatcatattcaaacacatagaaggctggagtgccctggac 728

Qy    1244 tccatttacttttgtggtggtcactctgaccacggtgggctttggtgattttgtggcaggg 1303
           |||||||  ||||||||  ||||||| || ||  | || ||||||||  |  || |||||
Db     729 gccatttattttgtggttatcactctaacaactattggatttggtgactacgttgcaggt 788

Qy    1304 ggaaacgctggcatcaattatcgggagtggtataagcccctagtgtggttttggatcctt 1363
           |||  || |   ||  | |||| ||| |  ||||||||  | ||||||||  |||||||||
Db     789 ggatccgat---attgaatatctggacttctataagcctgtcgtgtggttctggatcctt 845

Qy    1364 gttggccttgcctactttgcagctgtcctcagtatgatcggagattggctacgggttctg 1423
           || || ||||| |||||||| |||||||| || ||||| ||||||||||| || ||  |
Db     846 gtagggcttgcttactttgctgctgtcctgagcatgattggagattggctccgagtgata 905

Qy    1424 tccaaaaagacaaaagaagaggtgggtgaaatcaaggcccatgcggcagagtggaaggcc 1483
           || ||||||||||||||||||||||| ||  |||  || || || || |||||||  |||
Db     906 tctaaaaagacaaaagaagaggtgggagagttcagagcacacgctgctgagtggacagcc 965

Qy    1484 aatgtcacggctgagttccgggagacacggcgaaggctcagcgtggagatccacgataag 1543
           || ||||| || || |||   || ||  || |  | || || ||||||||  | || |||
Db     966 aacgtcacagccgaattcaaagaaaccaggaggcgactgagtgtggagatttatgacaag 1025

Qy    1544 ctgcagcgggcggccaccatc 1564
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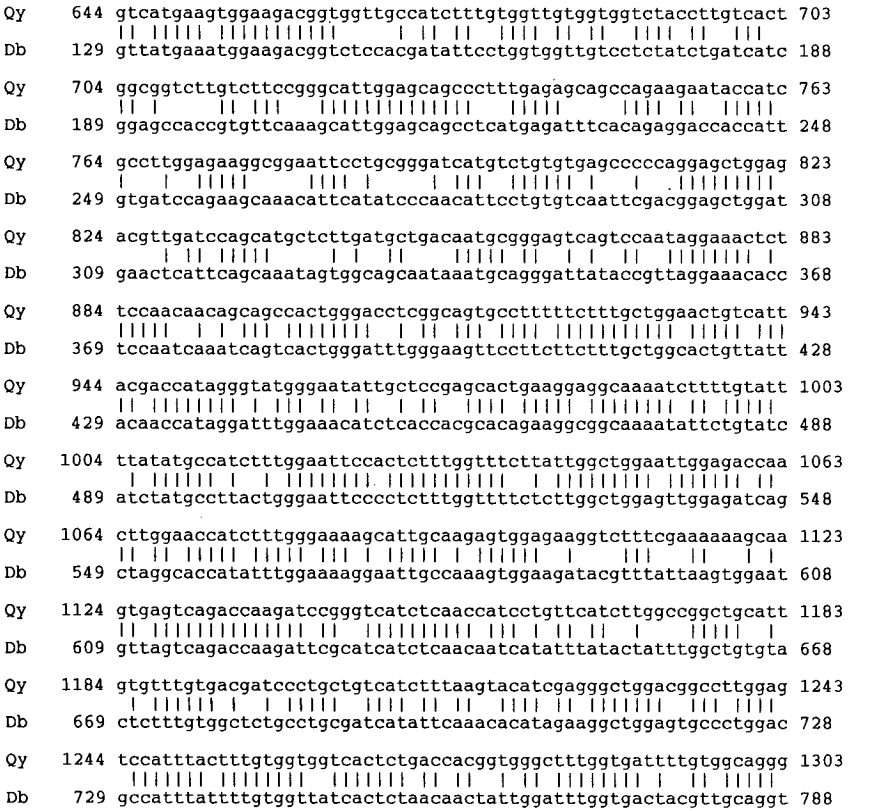
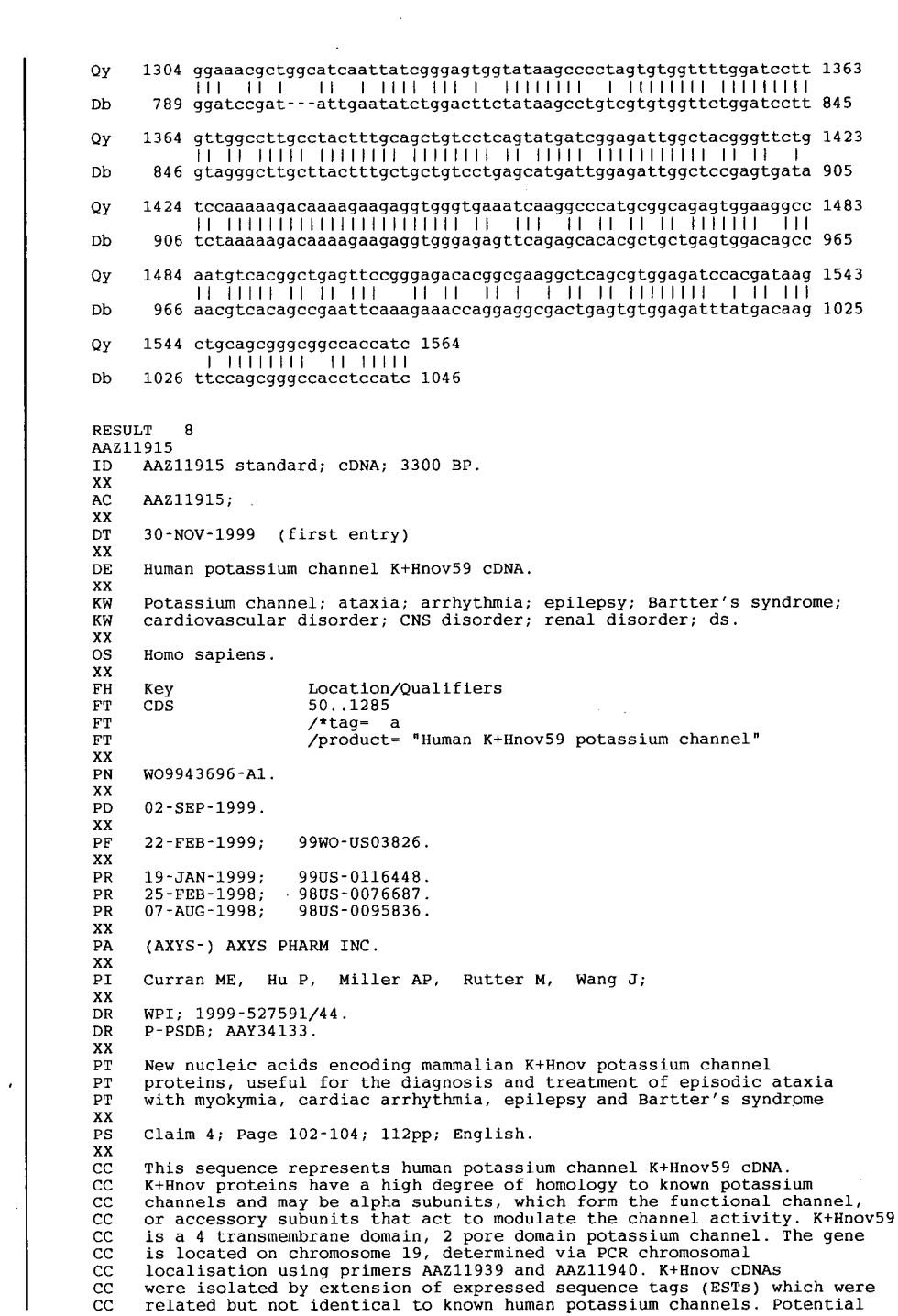
Db    1026 ttccagcgggccacctccatc 1046


RESULT   7
AAC90412
ID   AAC90412 standard; cDNA; 1246 BP.
XX
AC   AAC90412;
XX
DT   19-MAR-2001  (first entry)
XX
DE   Human TREK coding sequence.
XX
KW   Human; TREK; 2P domain potassium channel; resting membrane potential;
KW   neuronal excitability; neurotransmitter release modulation; epilepsy;
KW   neurological disorder; sleep-related disorder; cognitive dysfunction;
KW   attention deficit disorder; addiction; anxiety; phobia;
KW   Parkinson's chorea; Huntington's chorea; cerebral palsy; incontinence;
KW   erectile dysfunction; alopecia; ss.
XX
OS   Homo sapiens.
XX
PN   WO200072863-A2.
XX
PD   07-DEC-2000.
XX
PF   01-JUN-2000; 2000WO-GB02107.
XX
PR   01-JUN-1999;   99GB-0012733.
XX
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Hervieu GJ,  Meadows HJ,  Randall AD;
```

XX
DR WPI; 2001-080422/09.
DR P-PSDB; AAB50044.
XX
PT Use of human TREK1 polypeptide, polynucleotides encoding them and
PT modulators of h-TREK1 polypeptides for treating epilepsy, sleep-related
PT disorders, addiction and dyskinesias including Parkinson's and
PT Huntington's chorea -
XX
PS Claim 12; Page 29; 35pp; English.
XX
CC The present sequence is the coding sequence for human TREK1 (h-TREK1).
CC h-TREK1 is a member of the 2P domain potassium channel family of proteins
CC which play a part in the control of resting membrane potential.
CC Modulation of these channels will therefore affect neuronal excitability,
CC thereby leading to a modulation of neurotransmitter release and activity
CC of neuronal networks. Such modulation therefore may be useful for the
CC treatment of certain neurological conditions such as epilepsy,
CC sleep-related disorders, cognitive dysfunction, attention deficit
CC disorder, addiction, anxiety/phobia, Parkinson's and Huntington's chorea,
CC cerebral palsy, incontinence, erectile dysfunction or alopecia.
XX
SQ Sequence 1246 BP; 335 A; 280 C; 302 G; 329 T; 0 other;

Query Match 22.7%; Score 468.2; DB 22; Length 1246;
Best Local Similarity 70.0%; Pred. No. 6.5e-110;
Matches 645; Conservative 0; Mismatches 273; Indels 3; Gaps 1;





RESULT 8
AAZ11915
ID AAZ11915 standard; cDNA; 3300 BP.
XX
AC AAZ11915;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human potassium channel K+Hnov59 cDNA.
XX
KW Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;
KW cardiovascular disorder; CNS disorder; renal disorder; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 50..1285
FT /*tag= a
FT /product= "Human K+Hnov59 potassium channel"
XX
PN WO9943696-A1.
XX
PD 02-SEP-1999.
XX
PF 22-FEB-1999; 99WO-US03826.
XX
PR 19-JAN-1999; 99US-0116448.
PR 25-FEB-1998; 98US-0076687.
PR 07-AUG-1998; 98US-0095836.
XX
PA (AXYS-) AXYS PHARM INC.
XX
PI Curran ME, Hu P, Miller AP, Rutter M, Wang J;
XX
DR WPI; 1999-527591/44.
DR P-PSDB; AAY34133.
XX
PT New nucleic acids encoding mammalian K+Hnov potassium channel
PT proteins, useful for the diagnosis and treatment of episodic ataxia
PT with myokymia, cardiac arrhythmia, epilepsy and Bartter's syndrome
XX
PS Claim 4; Page 102-104; 112pp; English.
XX
CC This sequence represents human potassium channel K+Hnov59 cDNA.
CC K+Hnov proteins have a high degree of homology to known potassium
CC channels and may be alpha subunits, which form the functional channel,
CC or accessory subunits that act to modulate the channel activity. K+Hnov59
CC is a 4 transmembrane domain, 2 pore domain potassium channel. The gene
CC is located on chromosome 19, determined via PCR chromosomal
CC localisation using primers AAZ11939 and AAZ11940. K+Hnov cDNAs
CC were isolated by extension of expressed sequence tags (ESTs) which were
CC related but not identical to known human potassium channels. Potential

CC polymorphisms detected as sequence variants between multiple
CC independent clones. Potassium channels have critical roles in various
CC cell types and biochemical pathways. Defective potassium channels are
CC known to cause four human diseases: episodic ataxia with myokymia;
CC cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome.
CC As potassium channels are critical components of virtually all cells,
CC it is likely that abnormal potassium channels are also implicated in
CC certain renal, cardiovascular and central nervous system (CNS)
CC disorders. Nucleotides encoding K+Hnov proteins may be used for
CC identifying homologous or related proteins and the DNA sequences encoding
CC them. They may be used to produce compositions that modulate the
CC expression and function of the K+Hnov protein and in studying the
CC biochemical pathways associated with it. They may also be used for the
CC recombinant production of K+Hnov protein in fermentation cultures.
CC Additionally, such nucleotides may be used in gene therapy protocols for
CC the treatment of diseases associated with abnormal potassium channels.
XX
SQ Sequence 3300 BP; 997 A; 629 C; 680 G; 994 T; 0 other;

Query Match 22.7%; Score 468.2; DB 20; Length 3300;
Best Local Similarity 70.0%; Pred. No. 1e-109;
Matches 645; Conservative 0; Mismatches 273; Indels 3; Gaps 1;

```
Qy    644 gtcatgaagtggaagacggtggttgccatctttgtggttgtggtggtctaccttgtcact 703
          || ||||| ||||||||||     | || ||  |||| || ||  |||| ||  |||
Db    170 gttatgaaatggaagacggtctccacgatattcctggtggttgtcctctatctgatcatc 229

Qy    704 ggcggtcttgtcttccgggcattggagcagccctttgagagcagccagaagaataccatc 763
          || |     || |||   ||||||||||||||   |||||     |||| ||  |||||
Db    230 ggagccaccgtgttcaaagcattggagcagcctcatgagatttcacagaggaccaccatt 289

Qy    764 gccttggagaaggcggaattcctgcgggatcatgtctgtgtgagcccccaggagctggag 823
          |   | |||||     |||| |     | |||  |||||| |   |   |||||||||
Db    290 gtgatccagaagcaaacattcatatcccaacattcctgtgtcaattcgacggagctggat 349

Qy    824 acgttgatccagcatgctcttgatgctgacaatgcgggagtcagtccaataggaaactct 883
            | || |||||     | |  ||    ||||| ||  | |  ||  |||||||| |
Db    350 gaactcattcagcaaatagtggcagcaataaatgcagggattataccgttaggaaacacc 409

Qy    884 tccaacaacagcagccactgggacctcggcagtgccttttttctttgctggaactgtcatt 943
          |||||  | | ||| |||||||||  | || ||| |||| ||||||||||| ||||| |||
Db    410 tccaatcaaatcagtcactgggatttgggaagttccttcttctttgctggcactgttatt 469

Qy    944 acgaccatagggtatgggaatattgctccgagcactgaaggaggcaaaatcttttgtatt 1003
          || |||||||| | ||| || ||  | ||  |||| ||||| |||||||| || |||||
Db    470 acaaccataggatttggaaacatctcaccacgcacagaaggcggcaaaatattctgtatc 529

Qy   1004 ttatatgccatctttggaattccactctttggtttcttattggctggaattggagaccaa 1063
           | |||||| |  | |||||||| ||||||||||  | |||||||| |||||| ||
Db    530 atctatgccttactgggaattcccctctttggttttctcttggctggagttggagatcag 589

Qy   1064 cttggaaccatctttgggaaaagcattgcaagagtggagaaggtctttcgaaaaaagcaa 1123
          || || ||||| ||||| ||| | ||||| | ||||||  |    |||  ||   | |
Db    590 ctaggcaccatatttggaaaaggaattgccaaagtggaagatacgtttattaagtggaat 649

Qy   1124 gtgagtcagaccaagatccgggtcatctcaaccatcctgttcatcttggccggctgcatt 1183
          || |||||||||||||| ||  |||||||||| ||| | || ||  |    |||||  |
Db    650 gttagtcagaccaagattcgcatcatctcaacaatcatatttatactatttggctgtgta 709

Qy   1184 gtgtttgtgacgatccctgctgtcatctttaagtacatcgagggctggacggccttggag 1243
           | |||||| |  | |||||  |||| || ||  |||| || |||||||  ||| ||||
Db    710 ctctttgtggctctgcctgcgatcatattcaaacacatagaaggctggagtgccctggac 769

Qy   1244 tccatttacttttgtggtggtcactctgaccacggtgggctttggtgattttgtggcaggg 1303
           |||||||| ||||||||  |||||||| || ||  | || |||||||| |  || |||||
Db    770 gccatttatttttgtggttatcactctaacaactattggatttggtgactacgttgcaggt 829

Qy   1304 ggaaacgctggcatcaattatcgggagtggtataagcccctagtgtggttttggatcctt 1363
          |||  || |   ||  | |||| ||| |  ||||||||  | |||||||| |||||||||
Db    830 ggatccgat---attgaatatctggacttctataagcctgtcgtgtggttctggatcctt 886

Qy   1364 gttggccttgcctactttgcagctgtcctcagtatgatcggagattggctacgggttctg 1423
```

```
          || || ||||| |||||||| |||||||| || ||||| |||||||||| || ||  |
Db    887 gtagggcttgcttactttgctgctgtcctgagcatgattggagattggctccgagtgata 946

Qy   1424 tccaaaaagacaaaagaagaggtgggtgaaatcaaggcccatgcggcagagtggaaggcc 1483
          || ||||||||||||||||||||||| ||  |||  || || || || |||||||  |||
Db    947 tctaaaaagacaaaagaagaggtgggagagttcagagcacacgctgctgagtggacagcc 1006

Qy   1484 aatgtcacggctgagttccgggagacacggcgaaggctcagcgtggagatccacgataag 1543
          || ||||| || || |||   || ||  || |  | || || ||||||||  | || |||
Db    1007 aacgtcacagccgaattcaaagaaaccaggaggcgactgagtgtggagatttatgacaag 1066

Qy   1544 ctgcagcgggcggccaccatc 1564
           | |||||||| || |||||
Db    1067 ttccagcgggccacctccatc 1087
```

RESULT 9
AAZ10607
ID AAZ10607 standard; cDNA; 1993 BP.
XX
AC AAZ10607;
XX
DT 18-NOV-1999 (first entry)
XX
DE cDNA encoding a mechanically sensitive potassium channel protein TREK-1.
XX
KW Mechanically sensitive potassium channel protein; TREK-1;
KW polyunsaturated fatty acid; arachidonic acid; riluzole; heart disease;
KW nervous system disease; epilepsy; cardiovascular disease; arrhythmia;
KW neurodegeneration; ischemia; anoxia; hormone secretion abnormality;
KW muscular disease; ds.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 484..1596
FT /*tag= a
XX
PN WO9945108-A2.
XX
PD 10-SEP-1999.
XX
PF 23-FEB-1999; 99WO-FR00404.
XX
PR 05-MAR-1998; 98FR-0002725.
XX
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Honore E, Fink M, Lazdunski M, Lesage F, Duprat F;
XX
DR WPI; 1999-551038/46.
DR P-PSDB; AAY30648.
XX
PT New mechanically sensitive potassium channel, used to screen for
PT specific modulators, potential therapeutic agents for heart and nervous
PT system disorders -
XX
PS Claim 7; Page 23-25; 40pp; French.
XX
CC The present sequence encodes a mechanically sensitive potassium
CC channel protein designated TREK-1. The protein is activated by
CC polyunsaturated fatty acids, particularly arachidonic acid, and by
CC riluzole. The protein is used to screen for specific modulators which
CC are useful for treating or preventing diseases of the heart and nervous
CC systems in humans and animals, e.g. epilepsy, cardiovascular disease
CC (arrhythmia), neurodegeneration (particularly where associated with
CC ischemia or anoxia), abnormalities of hormone secretion and muscular
CC disease. The protein itself may be used to treat these diseases.
CC Antibodies specific for the protein are used to detect it in tissues,
CC also as therapeutic inhibitors or activators.
XX
SQ Sequence 1993 BP; 426 A; 570 C; 561 G; 436 T; 0 other;

```
  Query Match             22.7%;  Score 468;  DB 20;  Length 1993;
  Best Local Similarity   67.4%;  Pred. No. 9e-110;
  Matches  692;  Conservative    0;  Mismatches  325;  Indels    9;  Gaps    2;

Qy     538 gcaacccccggctccggctccgactccaactccgcgcctgtccatttcctcccgagccac 597
           | | |||  | || | |||| ||   | |  ||| | || ||  | || ||   | ||||
Db     504 ggatcccaagtctgctgctcagaactccaaaccgaggctctcattctcttcaaaacccac 563

Qy     598 agtggtagccaggatggaaggcacctcccaaggggcttgcagaccgtcatgaagtggaa 657
           ||| | ||      || | |    |  |          | || ||||| |||||
Db     564 cgtgcttgcttcccgggtggagagtgactcgg------ccattaatgttatgaaatggaa 617

Qy     658 gacggtggttgccatctttgtggttgtggtggtctaccttgtcactggcggtcttgtctt 717
           ||| ||     | || ||  |||| || ||  |||||||  |||  || |     || ||
Db     618 gacagtctccacgattttcctggtggtcgtcctctacctgatcatcggagccgcggtgtt 677

Qy     718 ccgggcattggagcagccctttgagagcagccagaagaataccatcgccttggagaaggc 777
           |  ||||||||||||||||    ||||    ||||| ||  |||||  |   |  |||||
Db     678 caaggcattggagcagcctcaggagatttcccagaggaccaccattgtgatccagaagca 737

Qy     778 ggaattcctgcgggatcatgtctgtgtgagcccccaggagctggagacgttgatccagca 837
           |   ||| |     | |||| ||| || | | ||   ||||||||     | ||||||||
Db     738 gaccttcatagcccagcatgcctgcgtcaactccaccgagctggacgaactcatccagca 797

Qy     838 tgctcttgatgctgacaatgcgggagtcagtccaataggaaactcttccaacaacagcag 897
           | |  ||    || || ||  | |  ||  ||||||||   |||||  |    ||
Db     798 aatagtggcagcaataaacgcagggattatccccttaggaaacagctccaatcaagttag 857

Qy     898 ccactgggacctcggcagtgccttttttctttgctggaactgtcattacgaccatagggta 957
           ||||||||||||||| ||  | || ||||||||||| ||||| || || ||||||||| |
Db     858 tcactgggacctcggaagctctttcttctttgctggtactgttatcacaaccataggatt 917

Qy     958 tgggaatattgctccgagcactgaaggaggcaaaatcttttgtattttatatgccatctt 1017
           ||| || ||  | ||  | |||||||| || ||||| || || ||  | ||||||  |  |
Db     918 tggaaacatctccccacgaactgaaggtggaaaaatattctgcatcatctatgccttgct 977

Qy    1018 tggaattccactctttggtttcttattggctggaattggagaccaacttggaaccatctt 1077
           ||||||||  |||||||| ||  || |||||||  |||| || || || ||||| || ||
Db     978 gggaattcccctctttggctttctactggctggggttggtgatcagctaggaactatatt 1037

Qy    1078 tgggaaaagcattgcaagagtggagaaggtctttcgaaaaaagcaagtgagtcagaccaa 1137
           ||| ||| | ||||| | ||||||  |    |||   ||   | | || ||||||||| ||
Db    1038 tggaaaaggaattgccaaagtggaagacacatttattaagtggaatgttagtcagacgaa 1097

Qy    1138 gatccgggtcatctcaaccatcctgttcatcttggccggctgcattgtgtttgtgacgat 1197
           ||| ||  ||||||| |||||| | |||||| ||   |||||  |  | |||||| |  |
Db    1098 gattcgtatcatctccaccatcatcttcatcctgtttggctgtgtcctctttgtggctct 1157

Qy    1198 ccctgctgtcatctttaagtacatcgagggctggacggccttggagtccatttacttttgt 1257
           |||||| ||||| || ||| |||| || |||||||  ||| ||||  | || || |||||
Db    1158 ccctgcggtcatattcaagcacatagaaggctggagcgccctggacgctatctattttgt 1217

Qy    1258 ggtggtcactctgaccacggtgggctttggtgattttgtggcaggggaaacgctggcat 1317
           ||| ||||||||||| ||  | || ||||| || |  |||||||| |||    | | |||
Db    1218 ggttatcactctgacgaccattggatttggagactacgtggcaggtgga---tcagacat 1274

Qy    1318 caattatcgggagtggtataagcccctagtgtggttttggatccttgttggccttgccta 1377
             | |||| ||| |  || |||||  | |||||||| |||||||| ||||| || |||||
Db    1275 tgaatatctggacttctacaagcctgtggtgtggttctggatcctcgttgggctggccta 1334

Qy    1378 ctttgcagctgtcctcagtatgatcggagattggctacgggttctgtccaaaaagacaaa 1437
           |||||||||||| || || ||||| || || ||||||||||  | || || |||||  ||
Db    1335 ctttgcagctgttctgagcatgattggggactggctacgggtgatctctaagaagacgaa 1394

Qy    1438 agaagaggtgggtgaaatcaaggcccatgcggcagagtggaaggccaatgtcacggctga 1497
           |||||||||| ||  |||  || ||||| || |||||||  ||||||||||||||| ||
Db    1395 ggaagaggtgggagagttcagagcgcatgccgctgagtggacagccaatgtcacggccga 1454

Qy    1498 gttccgggagacacggcgaaggctcagcgtggagatccacgataagctgcagcgggcggc 1557
           ||||  ||| ||  || |  |||| |||||||||||| |||| ||| | ||||| ||  |
Db    1455 gttcaaggaaacgaggaggcggctgagcgtggagatctacgacaagttccagcgtgccac 1514
```

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Qy    1558 caccat 1563
             || |
Db    1515 atccgt 1520
```

RESULT 10
AAZ00040
ID AAZ00040 standard; DNA; 1994 BP.
XX
AC AAZ00040;
XX
DT 12-OCT-1999 (first entry)
XX
DE Mouse h-TREK1 polynucleotide.
XX
KW h-TREK1; two pore potassium channel; inflammatory disease;
KW chromosome 1q32; ss.
XX
OS Mus musculus.
XX
FH Key   Location/Qualifiers
FT CDS   484..1719
FT   /*tag= a
FT   /product= "h-TREK1"
XX
PN WO9937762-A1.
XX
PD 29-JUL-1999.
XX
PF 02-DEC-1998; 98WO-EP07805.
XX
PR 09-OCT-1998; 98GB-0022135.
PR 27-JAN-1998; 98EP-0300570.
XX
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Chapman CG, Meadows HJ;
XX
DR WPI; 1999-469126/39.
DR P-PSDB; AAY28497.
XX
PT New two pore potassium channel used for, e.g. treatment of cancer,
PT pulmonary, cardiovascular and inflammatory diseases
XX
PS Claim 9; Page 25-26; 44pp; English.
XX
CC This sequence is the h-TREK1 polynucleotide from the mouse, encoding the
CC h-TREK1 polypeptide AAY28496. h-TREK1 is a two pore potassium channel.
CC The polynucleotide sequence of h-TREK1 can be used to diagnose a disease
CC or susceptibility to a disease related to expression or activity of
CC h-TREK1 polypeptides. The methods of diagnosis may be used in the
CC treatment of diseases including cancer, pulmonary, cardiovascular, and
CC inflammatory diseases, pain, psychiatric disorders including depression
CC and schizophrenia, neurodegenerative diseases including Alzheimer's,
CC stroke, and head trauma and neurological disorders including migraine.
XX
SQ Sequence 1994 BP; 426 A; 561 C; 561 G; 446 T; 0 other;

```
  Query Match             22.7%;  Score 468;  DB 20;  Length 1994;
  Best Local Similarity   67.4%;  Pred. No. 9e-110;
  Matches  692;  Conservative    0;  Mismatches  325;  Indels    9;  Gaps    2;

Qy     538 gcaacccccggctccggctccgactccaactccgcgcctgtccatttcctcccgagccac 597
           | | |||  | || | |||| ||   | |  ||| | || ||  | || ||   | ||||
Db     504 ggatcccaagtctgctgctcagaactccaaaccgaggctctcattctcttcaaaacccac 563

Qy     598 agtggtagccaggatggaaggcacctcccaaggggcttgcagaccgtcatgaagtggaa 657
           ||| | ||      || | |    |  |          | || ||||| |||||
Db     564 cgtgcttgcttcccgggtggagagtgactcgg------ccattaatgttatgaaatggaa 617

Qy     658 gacggtggttgccatctttgtggttgtggtggtctaccttgtcactggcggtcttgtctt 717
           ||| ||     | || ||  |||| || ||  |||||||  |||  || |     || ||
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Db    618 gacagtctccacgattttcctggtggtcgtcctctacctgatcatcggagccgcggtgtt 677

Qy    718 ccgggcattggagcagccctttgagagcagccagaagaataccatcgccttggagaaggc 777
          |  ||||||||||||||||    ||||    ||||| ||  ||||| |   |  |||||
Db    678 caaggcattggagcagcctcaggagatttcccagaggaccaccattgtgatccagaagca 737

Qy    778 ggaattcctgcgggatcatgtctgtgtgagccccccaggagctggagacgttgatccagca 837
          |   ||| |     | |||| ||| || | | ||   ||||||||     | ||||||||
Db    738 gaccttcatagcccagcatgcctgcgtcaactccaccgagctggacgaactcatccagca 797

Qy    838 tgctcttgatgctgacaatgcgggagtcagtccaataggaaactcttccaacaacagcag 897
              | |  ||    || || ||  | |  ||  ||||||||   |||||  |    ||
Db    798 aatagtggcagcaataaacgcagggattatccccttaggaaacagctccaatcaagttag 857

Qy    898 ccactgggacctcggcagtgccttttttctttgctggaactgtcattacgaccatagggta 957
           ||||||||||||||  ||  | || ||||||||||| ||||| || || ||||||||  |
Db    858 tcactgggacctccggaagctctttcttctttgctggtactgttatcacaaccataggatt 917

Qy    958 tgggaatattgctccgagcactgaaggaggcaaaatcttttgtattttatatgccatctt 1017
          ||| || ||  | ||  | |||||||| || ||||| || || ||  | ||||||  |  |
Db    918 tggaaacatctccccacgaactgaaggtggaaaaatattctgcatcatctatgccttgct 977

Qy   1018 tggaattccactctttggtttcttattggctggaattggagaccaacttggaaccatctt 1077
           ||||||||  ||||||||  ||  || |||||||  |||| || || || |||||  || ||
Db    978 gggaattcccctctttggctttctactggctggggttggtgatcagctaggaactatatt 1037

Qy   1078 tgggaaaagcattgcaagagtggagaaggtctttcgaaaaaagcaagtgagtcagaccaa 1137
          ||| ||| | ||||| | ||||||  |    |||   ||   | | || ||||||||| ||
Db   1038 tggaaaaggaattgccaaagtggaagacacatttattaagtggaatgttagtcagacgaa 1097

Qy   1138 gatccgggtcatctcaaccatcctgttcatcttggccggctgcattgtgtttgtgacgat 1197
          ||| ||  |||||||  |||||| | |||||| ||   |||||  |  | |||||| |  |
Db   1098 gattcgtatcatctccaccatcatcttcatcctgtttggctgtgtcctctttgtggctct 1157

Qy   1198 ccctgctgtcatctttaagtacatcgagggctggacggccttggagtccatttactttgt 1257
          ||||||  |||||  || ||| ||||  || |||||||  ||| ||||  | || || |||||
Db   1158 ccctgcggtcatattcaagcacatagaaggctggagcgccctggacgctatctattttgt 1217

Qy   1258 ggtggtcactctgaccacggtgggctttggtgattttgtggcaggggaaacgctggcat 1317
          |||  |||||||||| ||  | || |||||  || |  ||||||||  |||    | | |||
Db   1218 ggttatcactctgacgaccattggatttggagactacgtggcaggtgga---tcagacat 1274

Qy   1318 caattatcgggagtggtataagcccctagtgtggttttggatccttgttggccttgccta 1377
            | |||| ||| |  || |||||  | ||||||||  |||||||| |||||  || |||||
Db   1275 tgaatatctggacttctacaagcctgtggtgtggttctggatcctcgttgggctggccta 1334

Qy   1378 ctttgcagctgtcctcagtatgatcggagattggctacgggttctgtccaaaaagacaaa 1437
          ||||||||||||  || || |||||  || || ||||||||||  | || || |||||  ||
Db   1335 ctttgcagctgttctgagcatgattggggactggctacgggtgatctctaagaagacgaa 1394

Qy   1438 agaagaggtgggtgaaatcaaggcccatgcggcagagtggaaggccaatgtcacggctga 1497
           ||||||||||  ||  |||  || ||||| || |||||||  ||||||||||||||  ||
Db   1395 ggaagaggtgggagagttcagagcgcatgccgctgagtggacagccaatgtcacggccga 1454

Qy   1498 gttccgggagacacggcgaaggctcagcgtggagatccacgataagctgcagcgggcggc 1557
          ||||  ||| ||  || |  |||| |||||||||||| |||| ||| | ||||| ||  |
Db   1455 gttcaaggaaacgaggaggcggctgagcgtggagatctacgacaagttccagcgtgccac 1514

Qy   1558 caccat 1563
            || |
Db   1515 atccgt 1520


RESULT  11
AAS12169
ID   AAS12169 standard; cDNA; 2130 BP.
XX
AC   AAS12169;
XX
DT   21-NOV-2001  (first entry)
XX
DE   Human potassium ion channel TPKC1 cDNA.
XX
KW   Transmembrane potassium ion channel protein; inward potassium flux; ss;
KW   pest control; membrane potential; pesticide; antihelminthic; nematode;
KW   insect; TPKC1; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             178..1458
FT                   /*tag=  a
FT                   /product= "Human TPKC1 protein"
XX
PN   WO200161006-A2.
XX
PD   23-AUG-2001.
XX
PF   14-FEB-2001; 2001WO-US04680.
XX
PR   15-FEB-2000; 2000US-0503849.
XX
PA   (BADI ) BASF CORP.
XX
PI   Pausch MH;
XX
DR   WPI; 2001-536570/59.
DR   P-PSDB; AAU07618.
XX
PT   New polypeptide, a mutant potassium ion channel protein for improving
PT   inward potassium flux under acidic conditions  -
XX
PS   Example 15; Page 45-46; 131pp; English.
XX
CC   The invention relates to a mutant potassium ion channel protein, having
CC   four membrane spanning domains and two pore forming domains, comprising a
CC   mutation at the second pore forming domain. The expression of the mutant
CC   protein in a cell confers improved inward potassium flux and the ability
CC   to grow in the presence of potassium. Mutant proteins and their
CC   corresponding polynucleotide sequences can therefore be used to improve
CC   inward potassium flux into cells under acidic conditions by modulating
CC   the membrane potential using therapeutic agents. The sequences may be
CC   used to develop agonists and antagonists of potassium channel proteins in
CC   order to control pests such as nematodes and insects. This sequence
CC   represents a human cDNA encoding a transmembrane potassium ion channel
CC   protein, TPKC1.
XX
SQ   Sequence 2130 BP; 564 A; 480 C; 488 G; 593 T; 5 other;

  Query Match             22.2%;  Score 458.6;  DB 22;  Length 2130;
  Best Local Similarity   69.4%;  Pred. No. 2.4e-107;
  Matches  639;  Conservative    0;  Mismatches  279;  Indels    3;  Gaps    1;

Qy    644 gtcatgaagtggaagacggtggttgccatctttgtggttgtggtggtctaccttgtcact 703
          || ||||| ||||||||||     | || ||  |||| || ||  |||| ||  |||
Db    343 gttatgaaatggaagacggtctccacgatattcctggtggttgtcctctatctgatcatc 402

Qy    704 ggcggtcttgtcttccgggcattggagcagccctttgagagcagccagaagaataccatc 763
          || |     || |||   ||||||||||||||   |||||     |||| ||  |||||
Db    403 ggagccaccgtgttcaaagcattggagcagcctcatgagatttcacagaggaccaccatt 462

Qy    764 gccttggagaaggcggaattcctgcgggatcatgtctgtgtgagcccccaggagctggag 823
          |   |  |||||     |||| |     | |||  |||||| |   |   |||||||||
Db    463 gtgatccagaagcaaacattcatatcccaacattcctgtgtcaattcgacggagctggat 522

Qy    824 acgttgatccagcatgctcttgatgctgacaatgcgggagtcagtccaataggaaactct 883
              | || |||||     | |  ||    ||||| ||  | |  ||  |||||||| |
Db    523 gaactcattcagcaaatagtggcagcaataaatgcagggattataccgttaggaaacacc 582

Qy    884 tccaacaacagcagccactgggacctcggcagtgccttttttctttgctggaactgtcatt 943
          |||||  | | ||| |||||||||  | || ||| |||| ||||||||||| ||||| |||
Db    583 tccaatcaaatcagtcactgggatttgggaagttccttcttctttgctggcactgttatt 642

Qy    944 acgaccatagggtatgggaatattgctccgagcactgaaggaggcaaaatcttttgtatt 1003
          || |||||||| | ||| || ||  | ||  |||| ||||| |||||||| || |||||
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Db    643 acaaccataggatttggaaacatctcaccacgcacagaaggcggcaaaatattctgtatc 702

Qy   1004 ttatatgccatctttggaattccactctttggtttcttattggctggaattggagaccaa 1063
          | |||||| |  | |||||||| ||||||||||  | |||||||| |||||||
Db    703 atctatgccttactgggaattcccctctttggttttctcttggctggagttggagatcag 762

Qy   1064 cttggaaccatctttgggaaaagcattgcaagagtggagaaggtctttcgaaaaaagcaa 1123
          || || ||||| ||||| ||| | ||||| | ||||||  |    |||   ||   | |
Db    763 ctaggcaccatatttggaaaaggaattgccaaagtggaagatacgtttattaagtggaat 822

Qy   1124 gtgagtcagaccaagatccgggtcatctcaaccatcctgttcatcttggccggctgcatt 1183
          || |||||||||||||| ||  |||||||||| ||| | || ||  |    |||||  |
Db    823 gttagtcagaccaagattcgcatcatctcaacaatcatatttatactatttggctgtgta 882

Qy   1184 gtgtttgtgacgatccctgctgtcatctttaagtacatcgagggctggacggccttggag 1243
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Db    883 ctctttgtggctctgcctgcgatcatattcaaacacatagaaggctggagtgccctggac 942

Qy   1244 tccatttacttttgtggtggtcactctgaccacggtgggctttggtgattttgtggcaggg 1303
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Db    943 gccatttatttttgtggttatcactctaacaactattggatttggtgactacgttgcaggt 1002

Qy   1304 ggaaacgctggcatcaattatcgggagtggtataagcccctagtgtggttttggatcctt 1363
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Db   1003 ggatccgat---attgaatatctggacttctataagcctgtcgtgtggttctggatcctt 1059

Qy   1364 gttggccttgcctactttgcagctgtcctcagtatgatcggagattggctacgggttctg 1423
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Qy   1424 tccaaaaagacaaaagaagaggtgggtgaaatcaaggcccatgcggcagagtggaaggcc 1483
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Db   1120 tctaaaaagacaaaagaagaggtgggagagttcagagcacacgctgctgagtggacagcc 1179

Qy   1484 aatgtcacggctgagttccgggagacacggcgaaggctcagcgtggagatccacgataag 1543
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Db   1180 aacgtcacagccgaattcaaagaaaccaggaggcgactgagtgtggagatttatgacaag 1239

Qy   1544 ctgcagcgggcggccaccatc 1564
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Db   1240 ttccagcgggccacctccatc 1260


RESULT 12
AAS12181
ID   AAS12181 standard; cDNA; 2130 BP.
XX
AC   AAS12181;
XX
DT   21-NOV-2001  (first entry)
XX
DE   Human potassium ion channel protein TPKC1 cDNA mutant #1.
XX
KW   Transmembrane potassium ion channel protein; inward potassium flux; ss;
KW   pest control; membrane potential; pesticide; antihelminthic; nematode;
KW   insect; TPKC1; human; mutant.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             178..1458
FT                   /*tag=  a
FT                   /product= "Human TPKC1 mutant protein #1"
FT   mutation        replace(943,G)
FT                   /*tag=  b
XX
PN   WO200161006-A2.
XX
PD   23-AUG-2001.
XX
PF   14-FEB-2001; 2001WO-US04680.
XX
PR   15-FEB-2000; 2000US-0503849.
XX
PA   (BADI ) BASF CORP.
XX
PI   Pausch MH;
XX
DR   WPI; 2001-536570/59.
DR   P-PSDB; AAU07622.
XX
PT   New polypeptide, a mutant potassium ion channel protein for improving
PT   inward potassium flux under acidic conditions  -
XX
PS   Claim 12; Page 121-122; 131pp; English.
XX
CC   The invention relates to a mutant potassium ion channel protein, having
CC   four membrane spanning domains and two pore forming domains, comprising a
CC   mutation at the second pore forming domain. The expression of the mutant
CC   protein in a cell confers improved inward potassium flux and the ability
CC   to grow in the presence of potassium. Mutant proteins and their
CC   corresponding polynucleotide sequences can therefore be used to improve
CC   inward potassium flux into cells under acidic conditions by modulating
CC   the membrane potential using therapeutic agents. The sequences may be
CC   used to develop agonists and antagonists of potassium channel proteins in
CC   order to control pests such as nematodes and insects. This sequence
CC   represents a human cDNA encoding a transmembrane potassium ion channel
CC   mutant TPKC1 protein.
XX
SQ   Sequence 2130 BP; 565 A; 480 C; 487 G; 593 T; 5 other;

  Query Match             22.2%;  Score 458.6;  DB 22;  Length 2130;
  Best Local Similarity   69.4%;  Pred. No. 2.4e-107;
  Matches  639;  Conservative    0;  Mismatches  279;  Indels    3;  Gaps    1;

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Qy    704 ggcggtcttgtcttccgggcattggagcagccctttgagagcagccagaagaataccatc 763
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Db    403 ggagccaccgtgttcaaagcattggagcagcctcatgagatttcacagaggaccaccatt 462

Qy    764 gccttggagaaggcggaattcctgcgggatcatgtctgtgtgagcccccaggagctggag 823
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Db    463 gtgatccagaagcaaacattcatatcccaacattcctgtgtcaattcgacggagctggat 522

Qy    824 acgttgatccagcatgctcttgatgctgacaatgcgggagtcagtccaataggaaactct 883
              | || |||||     | |  ||     |||||  ||  | |  ||  |||||||| |
Db    523 gaactcattcagcaaatagtggcagcaataaatgcagggattataccgttaggaaacacc 582

Qy    884 tccaacaacagcagccactgggacctcggcagtgccttttttctttgctggaactgtcatt 943
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Db    583 tccaatcaaatcagtcactgggatttgggaagttccttcttctttgctggcactgttatt 642

Qy    944 acgaccatagggtatgggaatattgctccgagcactgaaggaggcaaaatcttttgtatt 1003
          || |||||||| | ||| || ||  | ||  |||| ||||| |||||||| || |||||
Db    643 acaaccataggatttggaaacatctcaccacgcacagaaggcggcaaaatattctgtatc 702

Qy   1004 ttatatgccatctttggaattccactctttggtttcttattggctggaattggagaccaa 1063
          | |||||| |  | |||||||| ||||||||||  | |||||||| |||||||  ||
Db    703 atctatgccttactgggaattcccctctttggttttctcttggctggagttggagatcag 762

Qy   1064 cttggaaccatctttgggaaaagcattgcaagagtggagaaggtctttcgaaaaaagcaa 1123
          || || ||||| ||||| ||| | ||||| | ||||||  |    |||   ||   | |
Db    763 ctaggcaccatatttggaaaaggaattgccaaagtggaagatacgtttattaagtggaat 822

Qy   1124 gtgagtcagaccaagatccgggtcatctcaaccatcctgttcatcttggccggctgcatt 1183
          || |||||||||||||| ||  |||||||||| ||| | || ||  |    |||||  |
Db    823 gttagtcagaccaagattcgcatcatctcaacaatcatatttatactatttggctgtgta 882

Qy   1184 gtgtttgtgacgatccctgctgtcatctttaagtacatcgagggctggacggccttggag 1243
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Qy   1244 tccatttacttttgtggtggtcactctgaccacggtgggctttggtgattttgtggcaggg 1303
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Db    943 accatttattttgtggttatcactctaacaactattggatttggtgactacgttgcaggt 1002

Qy   1304 ggaaacgctggcatcaattatcgggagtggtataagcccctagtgtggttttggatcctt 1363
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Db   1003 ggatccgat---attgaatatctggacttctataagcctgtcgtgtggttctggatcctt 1059

Qy   1364 gttggccttgcctactttgcagctgtcctcagtatgatcggagattggctacgggttctg 1423
          || || ||||| |||||||| |||||||| || ||||| ||    | | | || ||  |
Db   1060 gtagggcttgcttactttgctgctgtcctgagcatgattgggagattggtccgagtgata 1119

Qy   1424 tccaaaaagacaaaagaagaggtgggtgaaatcaaggcccatgcggcagagtggaaggcc 1483
          || ||||||||||||||||||||| ||  |||  || || || || ||||||  |||
Db   1120 tctaaaaagacaaaagaagaggtgggagagttcagagcacacgctgctgagtggacagcc 1179

Qy   1484 aatgtcacggctgagttccgggagacacggcgaaggctcagcgtggagatccacgataag 1543
          || ||||| || || |||   || ||  || |  | || || |||||||  | || |||
Db   1180 aacgtcacagccgaattcaaagaaaccaggaggcgactgagtgtggagatttatgacaag 1239

Qy   1544 ctgcagcgggcggccaccatc 1564
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Db   1240 ttccagcgggccacctccatc 1260
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RESULT 13
AAS12182
ID AAS12182 standard; cDNA; 2130 BP.
XX
AC AAS12182;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human potassium ion channel protein TPKC1 cDNA mutant #2.
XX
KW Transmembrane potassium ion channel protein; inward potassium flux; ss;
KW pest control; membrane potential; pesticide; antihelminthic; nematode;
KW insect; TPKC1; human; mutant.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	CDS	178..1458
FT		/*tag= a
FT		/product= "Human TPKC1 mutant protein #2"
FT	mutation	replace(991,T)
FT		/*tag= b

XX
PN WO200161006-A2.
XX
PD 23-AUG-2001.
XX
PF 14-FEB-2001; 2001WO-US04680.
XX
PR 15-FEB-2000; 2000US-0503849.
XX
PA (BADI) BASF CORP.
XX
PI Pausch MH;
XX
DR WPI; 2001-536570/59.
DR P-PSDB; AAU07623.
XX
PT New polypeptide, a mutant potassium ion channel protein for improving
PT inward potassium flux under acidic conditions -
XX
PS Claim 12; Page 123-124; 131pp; English.
XX
CC The invention relates to a mutant potassium ion channel protein, having
CC four membrane spanning domains and two pore forming domains, comprising a
CC mutation at the second pore forming domain. The expression of the mutant
CC protein in a cell confers improved inward potassium flux and the ability
CC to grow in the presence of potassium. Mutant proteins and their
CC corresponding polynucleotide sequences can therefore be used to improve
CC inward potassium flux into cells under acidic conditions by modulating
CC the membrane potential using therapeutic agents. The sequences may be
CC used to develop agonists and antagonists of potassium channel proteins in
CC order to control pests such as nematodes and insects. This sequence
CC represents a human cDNA encoding a transmembrane potassium ion channel
CC mutant TPKC1 protein.
XX
SQ Sequence 2130 BP; 564 A; 481 C; 488 G; 592 T; 5 other;

Query Match 22.1%; Score 457; DB 22; Length 2130;
Best Local Similarity 69.3%; Pred. No. 6.2e-107;
Matches 638; Conservative 0; Mismatches 280; Indels 3; Gaps 1;

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Qy    644 gtcatgaagtggaagacggtggttgccatctttgtggttgtggtggtctaccttgtcact 703
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Db    343 gttatgaaatggaagacggtctccacgatattcctggtggttgtcctctatctgatcatc 402

Qy    704 ggcggtcttgtcttccgggcattggagcagccctttgagagcagccagaagaataccatc 763
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Db    403 ggagccaccgtgttcaaagcattggagcagcctcatgagatttcacagaggaccaccatt 462

Qy    764 gccttggagaaggcggaattcctgcgggatcatgtctgtgtgagcccccaggagctggag 823
          |   |  |||||     |||| |     | |||  |||||| |   |   |||||||||
Db    463 gtgatccagaagcaaacattcatatcccaacattcctgtgtcaattcgacggagctggat 522

Qy    824 acgttgatccagcatgctcttgatgctgacaatgcgggagtcagtccaataggaaactct 883
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Db    523 gaactcattcagcaaatagtggcagcaataaatgcagggattataccgttaggaaacacc 582

Qy    884 tccaacaacagcagccactgggacctcggcagtgccttttctttgctggaactgtcatt 943
          |||||  | | ||| ||||||||  | || ||| |||| ||||||||||| ||||| |||
Db    583 tccaatcaaatcagtcactgggatttgggaagttccttcttctttgctggcactgttatt 642

Qy    944 acgaccatagggtatgggaatattgctccgagcactgaaggaggcaaaatcttttgtatt 1003
          || |||||||| | ||| || ||  | ||  |||| ||||| |||||||| || |||||
Db    643 acaaccataggatttggaaacatctcaccacgcacagaaggcggcaaaatattctgtatc 702

Qy   1004 ttatatgccatctttggaattccactctttggtttcttattggctggaattggagaccaa 1063
           | |||||| |  | |||||||| ||||||||||  | |||||||| ||||||| ||
Db    703 atctatgccttactgggaattcccctctttggttttctcttggctggagttggagatcag 762

Qy   1064 cttggaaccatctttgggaaaagcattgcaagagtggagaaggtctttcgaaaaaagcaa 1123
          || || ||||| ||||| ||| | ||||| | ||||||  |    |||   ||   | |
Db    763 ctaggcaccatatttggaaaaggaattgccaaagtggaagatacgtttattaagtggaat 822

Qy   1124 gtgagtcagaccaagatccgggtcatctcaaccatcctgttcatcttggccggctgcatt 1183
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Db    823 gttagtcagaccaagattcgcatcatctcaacaatcatatttatactatttggctgtgta 882

Qy   1184 gtgtttgtgacgatccctgctgtcatctttaagtacatcgagggctggacggccttggag 1243
           | |||||| |  | |||||  |||| || ||  |||| || |||||||  ||| ||||
Db    883 ctctttgtggctctgcctgcgatcatattcaaacacatagaaggctggagtgccctggac 942

Qy   1244 tccatttacttttgtggtggtcactctgaccacggtgggctttggtgattttgtggcaggg 1303
          ||||||| ||||||||  |||||||| || ||  | || ||||||||    || |||||
Db    943 gccatttattttgtggttatcactctaacaactattggatttggtgaccacgttgcaggt 1002

Qy   1304 ggaaacgctggcatcaattatcgggagtggtataagcccctagtgtggttttggatcctt 1363
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Db   1003 ggatccgat---attgaatatctggacttctataagcctgtcgtgtggttctggatcctt 1059

Qy   1364 gttggccttgcctactttgcagctgtcctcagtatgatcggagattggctacgggttctg 1423
          || || ||||| |||||||| |||||||| || ||||| ||    | | | || ||  |
Db   1060 gtagggcttgcttactttgctgctgtcctgagcatgattgggagattggtccgagtgata 1119

Qy   1424 tccaaaaagacaaaagaagaggtgggtgaaatcaaggcccatgcggcagagtggaaggcc 1483
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Db   1120 tctaaaaagacaaaagaagaggtgggagagttcagagcacacgctgctgagtggacagcc 1179

Qy   1484 aatgtcacggctgagttccgggagacacggcgaaggctcagcgtggagatccacgataag 1543
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Db   1180 aacgtcacagccgaattcaaagaaaccaggaggcgactgagtgtggagatttatgacaag 1239

Qy   1544 ctgcagcgggcggccaccatc 1564
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Db   1240 ttccagcgggccacctccatc 1260


RESULT  14
AAS12184
ID   AAS12184 standard; cDNA; 2130 BP.
XX
AC   AAS12184;
XX
DT   21-NOV-2001  (first entry)
XX
DE   Human potassium ion channel protein TPKC1 cDNA mutant #4.
XX
KW   Transmembrane potassium ion channel protein; inward potassium flux; ss;
KW   pest control; membrane potential; pesticide; antihelminthic; nematode;
KW   insect; TPKC1; human; mutant.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             178..1458
FT                   /*tag=  a
FT                   /product= "Human TPKC1 mutant protein #4"
FT   mutation        replace(985,G)
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XX
PN   WO200161006-A2.
XX
PD   23-AUG-2001.
XX
PF   14-FEB-2001; 2001WO-US04680.
XX
PR   15-FEB-2000; 2000US-0503849.
XX
PA   (BADI ) BASF CORP.
XX
PI   Pausch MH;
XX
DR   WPI; 2001-536570/59.
DR   P-PSDB; AAU07625.
XX
PT   New polypeptide, a mutant potassium ion channel protein for improving
PT   inward potassium flux under acidic conditions  -
XX
PS   Claim 12; Page 126-127; 131pp; English.
XX
CC   The invention relates to a mutant potassium ion channel protein, having
CC   four membrane spanning domains and two pore forming domains, comprising a
CC   mutation at the second pore forming domain. The expression of the mutant
CC   protein in a cell confers improved inward potassium flux and the ability
CC   to grow in the presence of potassium. Mutant proteins and their
CC   corresponding polynucleotide sequences can therefore be used to improve
CC   inward potassium flux into cells under acidic conditions by modulating
CC   the membrane potential using therapeutic agents. The sequences may be
CC   used to develop agonists and antagonists of potassium channel proteins in
CC   order to control pests such as nematodes and insects. This sequence
CC   represents a human cDNA encoding a transmembrane potassium ion channel
CC   mutant TPKC1 protein.
XX
SQ   Sequence 2130 BP; 564 A; 481 C; 487 G; 593 T; 5 other;


  Query Match             22.1%;  Score 457;  DB 22;  Length 2130;
  Best Local Similarity   69.3%;  Pred. No. 6.2e-107;
  Matches  638;  Conservative    0;  Mismatches  280;  Indels    3;  Gaps    1;

Qy    644 gtcatgaagtggaagacggtggttgccatctttgtggttgtggtggtctaccttgtcact 703
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Qy    704 ggcggtcttgtcttccgggcattggagcagccctttgagagcagccagaagaataccatc 763
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Qy    764 gccttggagaaggcggaattcctgcgggatcatgtctgtgtgagcccccaggagctggag 823
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Db    463 gtgatccagaagcaaacattcatatcccaacattcctgtgtcaattcgacggagctggat 522

Qy    824 acgttgatccagcatgctcttgatgctgacaatgcgggagtcagtccaataggaaactct 883
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Qy    884 tccaacaacagcagccactgggacctcggcagtgccttttttctttgctggaactgtcatt 943
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Db    583 tccaatcaaatcagtcactgggatttgggaagttccttcttctttgctggcactgttatt 642

Qy    944 acgaccatagggtatgggaatattgctccgagcactgaaggaggcaaaatcttttgtatt 1003
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Db    643 acaaccataggatttggaaacatctcaccacgcacagaaggcggcaaaatattctgtatc 702

Qy   1004 ttatatgccatctttggaattccactctttggtttcttattggctggaattggagaccaa 1063
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Db    703 atctatgccttactgggaattcccctctttggttttctcttggctggagttggagatcag 762

Qy   1064 cttggaaccatctttgggaaaagcattgcaagagtggagaaggtctttcgaaaaaagcaa 1123
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Db    763 ctaggcaccatatttggaaaaggaattgccaaagtggaagatacgtttattaagtggaat 822

Qy   1124 gtgagtcagaccaagatccgggtcatctcaaccatcctgttcatcttggccggctgcatt 1183
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           | |||||| |  | |||||  |||| || ||  |||| || |||||||  ||| ||||
Db    883 ctctttgtggctctgcctgcgatcatattcaaacacatagaaggctggagtgccctggac 942

Qy   1244 tccatttacttttgtggtggtcactctgaccacggtgggctttggtgattttgtggcaggg 1303
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Db    943 gccatttatttttgtggttatcactctaacaactattggatttcgtgactacgttgcaggt 1002

Qy   1304 ggaaacgctggcatcaattatcgggagtggtataagcccctagtgtggttttggatccttt 1363
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Db   1003 ggatccgat---attgaatatctggacttctataagcctgtcgtgtggttctggatccttt 1059

Qy   1364 gttggccttgcctactttgcagctgtcctcagtatgatcggagattggctacgggttctg 1423
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Db   1060 gtagggcttgcttactttgctgctgtcctgagcatgattgggagattggtccgagtgata 1119

Qy   1424 tccaaaaagacaaaagaagaggtgggtgaaatcaaggcccatgcggcagagtggaaggcc 1483
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Db   1120 tctaaaaagacaaaagaagaggtgggagagttcagagcacacgctgctgagtggacagcc 1179

Qy   1484 aatgtcacggctgagttccgggagacacggcgaaggctcagcgtggagatccacgataag 1543
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Db   1180 aacgtcacagccgaattcaaagaaaccaggaggcgactgagtgtggagatttatgacaag 1239

Qy   1544 ctgcagcgggcggccaccatc 1564
           | ||||||||  || |||||
Db   1240 ttccagcgggccacctccatc 1260


RESULT  15
AAS12183
ID   AAS12183 standard; cDNA; 2130 BP.
XX
AC   AAS12183;
XX
DT   21-NOV-2001  (first entry)
XX
DE   Human potassium ion channel protein TPKC1 cDNA mutant #3.
XX
KW   Transmembrane potassium ion channel protein; inward potassium flux; ss;
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```
KW   pest control; membrane potential; pesticide; antihelminthic; nematode;
KW   insect; TPKC1; human; mutant.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             178..1458
FT                   /*tag= a
FT                   /product= "Human TPKC1 mutant protein #3"
FT   mutation        replace(991,T)
FT                   /*tag= b
FT   mutation        replace(998,C)
FT                   /*tag= c
XX
PN   WO200161006-A2.
XX
PD   23-AUG-2001.
XX
PF   14-FEB-2001; 2001WO-US04680.
XX
PR   15-FEB-2000; 2000US-0503849.
XX
PA   (BADI ) BASF CORP.
XX
PI   Pausch MH;
XX
DR   WPI; 2001-536570/59.
DR   P-PSDB; AAU07624.
XX
PT   New polypeptide, a mutant potassium ion channel protein for improving
PT   inward potassium flux under acidic conditions -
XX
PS   Claim 12; Page 124-125; 131pp; English.
XX
CC   The invention relates to a mutant potassium ion channel protein, having
CC   four membrane spanning domains and two pore forming domains, comprising a
CC   mutation at the second pore forming domain. The expression of the mutant
CC   protein in a cell confers improved inward potassium flux and the ability
CC   to grow in the presence of potassium. Mutant proteins and their
CC   corresponding polynucleotide sequences can therefore be used to improve
CC   inward potassium flux into cells under acidic conditions by modulating
CC   the membrane potential using therapeutic agents. The sequences may be
CC   used to develop agonists and antagonists of potassium channel proteins in
CC   order to control pests such as nematodes and insects. This sequence
CC   represents a human cDNA encoding a transmembrane potassium ion channel
CC   mutant TPKC1 protein.
XX
SQ   Sequence 2130 BP; 564 A; 480 C; 488 G; 593 T; 5 other;
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Query Match 22.1%; Score 455.4; DB 22; Length 2130;
Best Local Similarity 69.2%; Pred. No. 1.6e-106;
Matches 637; Conservative 0; Mismatches 281; Indels 3; Gaps 1;

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Qy    704 ggcggtcttgtcttccgggcattggagcagccctttgagagcagccagaagaataccatc 763
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Db    583 tccaatcaaatcagtcactgggatttgggaagttccttcttctttgctggcactgttatt 642

Qy    944 acgaccatagggtatgggaatattgctccgagcactgaaggaggcaaaatcttttgtatt 1003
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Qy   1244 tccatttactttgtggtggtcactctgaccacggtgggctttggtgattttgtggcaggg 1303
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Search completed: September 21, 2002, 08:38:25
Job time: 6926 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: September 21, 2002, 05:46:09 ; Search time 91.5 Seconds
(without alignments)
5543.532 Million cell updates/sec

Title: US-09-729-920-1
Perfect score: 2065
Sequence: 1 ggacactgacatggactgaa.....tacttgaagacagaaactaa 2065

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	468.2	22.7	1246	4	US-09-236-080-1	Sequence 1, Appli
2	468	22.7	1994	4	US-09-236-080-5	Sequence 5, Appli
3	181	8.8	321	4	US-09-236-080-3	Sequence 3, Appli
4	106.8	5.2	1894	3	US-08-749-816-1	Sequence 1, Appli
5	106.8	5.2	1894	4	US-09-144-914-1	Sequence 1, Appli
6	78.2	3.8	2514	4	US-09-144-914-3	Sequence 3, Appli
7	74.8	3.6	7218	1	US-08-232-463-14	Sequence 14, Appl
8	53.2	2.6	2441	1	US-08-332-312-1	Sequence 1, Appli
c 9	51.4	2.5	7218	1	US-08-232-463-14	Sequence 14, Appl
c 10	49	2.4	289	4	US-09-007-005-17	Sequence 17, Appl
c 11	49	2.4	289	4	US-09-244-796-17	Sequence 17, Appl
12	44.8	2.2	1011	1	US-08-332-312-3	Sequence 3, Appli
13	43.8	2.1	5511	3	US-08-928-361B-2	Sequence 2, Appli
14	43.8	2.1	7334	3	US-08-928-361B-1	Sequence 1, Appli
15	42.6	2.1	43280	2	US-08-804-227C-1	Sequence 1, Appli
16	42.4	2.1	1288	1	US-08-440-856A-9	Sequence 9, Appli
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18	41.4	2.0	4826	4	US-09-192-983-3	Sequence 3, Appli
19	40.4	2.0	198	5	PCT-US95-10668-1	Sequence 1, Appli
20	40.4	2.0	198	5	PCT-US95-10668-2	Sequence 2, Appli
21	40.4	2.0	198	5	PCT-US95-10668-3	Sequence 3, Appli
22	40.4	2.0	198	5	PCT-US95-10668-4	Sequence 4, Appli
23	40.2	1.9	1358	1	US-08-471-033-45	Sequence 45, Appl
24	40.2	1.9	1358	2	US-08-471-044-45	Sequence 45, Appl
25	40.2	1.9	1358	2	US-08-463-483A-45	Sequence 45, Appl
26	40.2	1.9	1358	2	US-08-471-046A-45	Sequence 45, Appl
27	40.2	1.9	1358	2	US-08-470-566B-45	Sequence 45, Appl
28	40.2	1.9	1358	2	US-08-469-334-45	Sequence 45, Appl
29	40.2	1.9	1358	3	US-09-300-529-45	Sequence 45, Appl
30	39.8	1.9	1995	1	US-08-425-069-3	Sequence 3, Appli
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32	39.6	1.9	1241	1	US-08-471-033-39	Sequence 39, Appl
33	39.6	1.9	1241	1	US-08-471-033-42	Sequence 42, Appl
34	39.6	1.9	1241	2	US-08-471-044-39	Sequence 39, Appl
35	39.6	1.9	1241	2	US-08-471-044-42	Sequence 42, Appl
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37	39.6	1.9	1241	2	US-08-463-483A-42	Sequence 42, Appl
38	39.6	1.9	1241	2	US-08-471-046A-39	Sequence 39, Appl
39	39.6	1.9	1241	2	US-08-471-046A-42	Sequence 42, Appl
40	39.6	1.9	1241	2	US-08-470-566B-39	Sequence 39, Appl
41	39.6	1.9	1241	2	US-08-470-566B-42	Sequence 42, Appl
42	39.6	1.9	1241	2	US-08-469-334-39	Sequence 39, Appl
43	39.6	1.9	1241	2	US-08-469-334-42	Sequence 42, Appl
44	39.6	1.9	1241	3	US-09-300-529-39	Sequence 39, Appl
45	39.6	1.9	1241	3	US-09-300-529-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1
US-09-236-080-1
; Sequence 1, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217el Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236,080
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1246
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-236-080-1

Query Match 22.7%; Score 468.2; DB 4; Length 1246;
Best Local Similarity 70.0%; Pred. No. 4.4e-121;
Matches 645; Conservative 0; Mismatches 273; Indels 3; Gaps 1;

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Qy    704 ggcggtcttgtcttccgggcattggagcagccctttgagagcagccagaagaataccatc 763
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Qy    764 gccttggagaaggcggaattcctgcgggatcatgtctgtgtgagcccccaggagctggag 823
          |   | |||||     |||| |     | |||  |||||| |   |   |||||||||
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Qy    824 acgttgatccagcatgctcttgatgctgacaatgcgggagtcagtccaataggaaactct 883
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Qy    944 acgaccatagggtatgggaatattgctccgagcactgaaggaggcaaaatcttttgtatt 1003
          || |||||||| | ||| || ||  | ||  |||| ||||| |||||||| || |||||
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Qy   1124 gtgagtcagaccaagatccgggtcatctcaaccatcctgttcatcttggccggctgcatt 1183
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RESULT 2
US-09-236-080-5
; Sequence 5, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217el Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236,080
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1994
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-236-080-5

Query Match 22.7%; Score 468; DB 4; Length 1994;
Best Local Similarity 67.4%; Pred. No. 6.4e-121;
Matches 692; Conservative 0; Mismatches 325; Indels 9; Gaps 2;

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Qy    598 agtggtagccaggatggaaggcacctcccaaggggcttgcagaccgtcatgaagtggaa 657
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Qy    658 gacggtggttgccatctttgtggttgtggtggtctaccttgtcactggcggtcttgtctt 717
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Qy    718 ccgggcattggagcagccctttgagagcagccagaagaataccatcgccttggagaaggc 777
Db    678 caaggcattggagcagcctcaggagatttcccagaggaccaccattgtgatccagaagca 737

Qy    778 ggaattcctgcgggatcatgtctgtgtgagcccccaggagctggagacgttgatccagca 837
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Qy    838 tgctcttgatgctgacaatgcgggagtcagtccaataggaaactcttccaacaacagcag 897
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Qy    898 ccactgggacctcggcagtgccttttttctttgctggaactgtcattacgaccatagggta 957
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RESULT 3
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; Sequence 3, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217el Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236,080

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;  CURRENT FILING DATE: 1999-01-25
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-236-080-3


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Qy    938 gtcattacgaccatagggtatgggaatattgctccgagcactgaaggaggcaaaatcttt 997
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Qy   1058 gaccaacttggaaccatctttgggaaaagcattgcaagagtggagaaggtctttcgaaaa 1117
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Qy   1118 aagcaagtgagtcagaccaagatccgggtcatctcaaccatcctgttcatcttggccggc 1177
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RESULT   4
US-08-749-816-1
; Sequence 1, Application US/08749816
; Patent No. 6013470
;  GENERAL INFORMATION:
;    APPLICANT:  Lesage, Florian
;    APPLICANT:  Guillemare, Eric
;    APPLICANT:  Fink, Michel
;    APPLICANT:  Duprat, Fabrice
;    APPLICANT:  Lazdunki, Michel
;    APPLICANT:  Romey, Georges
;    APPLICANT:  Barhanin, Jacques
;    TITLE OF INVENTION:  FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
;    TITLE OF INVENTION:  THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
;    TITLE OF INVENTION:  OF DRUGS
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  WEISER & ASSOCIATES
;      STREET:  230 South Fifteenth Street, Suite 500
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/749,816
;      FILING DATE:  15-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weiser, Gerard J.
;      REGISTRATION NUMBER:  19,763
;      REFERENCE/DOCKET NUMBER:  989.6351P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-875-8383
;      TELEFAX:  215-875-8394
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1894 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  183..1190
US-08-749-816-1


  Query Match             5.2%;  Score 106.8;  DB 3;  Length 1894;
  Best Local Similarity   49.3%;  Pred. No. 5.2e-20;
  Matches  338;  Conservative    0;  Mismatches  342;  Indels    6;  Gaps    2;

Qy    687 tggtctaccttgtcactggcggtcttgtcttccgggcattggagcagccccttgagagca 746
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Db    274 TGCTCTACCTGGTCTTCGGCGCAGTGGTCTTCTCCTCGGTGGAGCTGCCCTATGAGGACC 333

Qy    747 gccagaagaataccatcgccttggagaaggcggaattcctgcgggatcatgtctgtgtga 806
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Db    334 TGCTGCGCCAGGAGCTGCGCAAGCTGAAGCGACGCTTCTTGGAGGAGCACGAGTGCCTGT 393

Qy    807 gcccccaggagctggagacgttgatccagcatgctcttgatgctgacaatgcgggagtca 866
              ||| |||||||  |||  |    |  |  || || ||   |||    || ||
Db    394 CTGAGCAGCAGCTGGAGCAGTTCCTGGGCCGGGTGCTGGAGGCCAGCAACTACGGCGTGT 453

Qy    867 gtccaataggaaactcttccaacaacagcagccactgggacctcggcagtgccttttttct 926
            |  | ||| | ||   |||| | |   |||||||| ||  |   ||  | ||||
Db    454 CGGTGCTCAGCAACGCCTCGGGCAACTGGA---ACTGGGACTTCACCTCCGCGCTCTTCT 510

Qy    927 ttgctggaactgtcattacgaccatagggtatgggaatattgctccgagcactgaaggag 986
          | ||  | || ||  |  | |||| ||| |||||  | |  |  ||    | || ||||
Db    511 TCGCCAGCACCGTGCTCTCCACCACAGGTTATGGCCACACCGTGCCCTTGTCAGATGGAG 570

Qy    987 gcaaaatcttttgtattttatatgccatctttggaattccactctttggtttcttattgg 1046
          | ||   ||| || ||  | ||  || || |||| |||||  ||       | ||  ||
Db    571 GTAAGGCCTTCTGCATCATCTACTCCGTCATTGGCATTCCCTTCACCCTCCTGTTCCTGA 630

Qy   1047 ctggaattggagaccaacttggaaccatctttgggaaaagcattgcaagagtggagaaagg 1106
          | |    ||  | ||| |     ||| |    |  |  |||   |     |  |
Db    631 CGG---CTGTGGTCCAGCGCATCACCGTGCACGTCACCCGCAGGCCGGTCCTCTACTTCC 687

Qy   1107 tctttcgaaaaaagcaagtgagtcagaccaagatccgggtcatctcaaccatcctgttca 1166
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Db    688 ACATCCGCTGGGGCTTCTCCAAGCAGGTGGTGGCCATCGTCCATGCCGTGCTCCTTGGGT 747

Qy   1167 tcttggccggctgcattgtgtttgtgacgatccctgctgtcatctttaagtacatcgagg 1226
          |  |  | |  | |    | ||  | |      | |||||| |||          || |
Db    748 TTGTCACTGTGTCCTGCTTCTTCTTCATCCCGGCCGCTGTCTTCTCAGTCCTGGAGGATG 807

Qy   1227 gctggacggccttggagtccatttactttgtggtggtcactctgaccacggtgggctttg 1286
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Db    808 ACTGGAACTTCCTGGAATCCTTTTATTTTTGTTTTATTTCCCTGAGCACCATTGGCCTGG 867

Qy   1287 gtgattttgtggcaggggggaaacgctggcatcaattatcgggagtggtataagcccctag 1346
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Db    868 GGGATTATGTGCCTGGGGAAGGCTACAATCAAAAATTCAGAGAGCTCTATAAGATTGGGA 927

Qy   1347 tgtggttttggatccttgttggcctt 1372
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Db    928 TCACGTGTTACCTGCTACTTGGCCTT 953


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US-09-144-914-1
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; Sequence 1, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
;  APPLICANT: Duprat, Fabrice
;  APPLICANT: Lesage, Florian
;  APPLICANT: Fink, Michel
;  APPLICANT: Lazdunski, Michel
;  TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
;  TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
;  FILE REFERENCE: 989.6705CIP
;  CURRENT APPLICATION NUMBER: US/09/144,914
;  CURRENT FILING DATE: 1998-09-01
;  EARLIER APPLICATION NUMBER: 08/749,816
;  EARLIER FILING DATE: 1996-11-15
;  EARLIER APPLICATION NUMBER: 60/095,234
;  EARLIER FILING DATE: 1998-08-04
;  EARLIER APPLICATION NUMBER: FR 96/01565
;  EARLIER FILING DATE: 1996-02-08
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1894
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (183)..(1190)
;   FEATURE:
;   OTHER INFORMATION: TWIK-1
US-09-144-914-1


  Query Match             5.2%;  Score 106.8;  DB 4;  Length 1894;
  Best Local Similarity   49.3%;  Pred. No. 5.2e-20;
  Matches  338;  Conservative    0;  Mismatches  342;  Indels    6;  Gaps    2;

Qy    687 tggtctaccttgtcactggcggtcttgtcttccgggcattggagcagccctttgagagca 746
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Db    274 tgctctacctggtcttcggcgcagtggtcttctcctcggtggagctgccctatgaggacc 333

Qy    747 gccagaagaataccatcgccttggagaaggcggaattcctgcgggatcatgtctgtgtga 806
            | |    |     |   |  |  ||||      ||| ||  ||| || |  ||  ||
Db    334 tgctgcgccaggagctgcgcaagctgaagcgacgcttcttggaggagcacgagtgcctgt 393

Qy    807 gcccccaggagctggagacgttgatccagcatgctcttgatgctgacaatgcgggagtca 866
              ||| |||||||  |||  |    |  |  || || ||   |||     || ||
Db    394 ctgagcagcagctggagcagttcctgggccgggtgctggaggccagcaactacggcgtgt 453

Qy    867 gtccaataggaaactcttccaacaacagcagccactgggacctcggcagtgccttttct 926
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Db    454 cggtgctcagcaacgcctcgggcaactgga---actgggacttcacctccgcgctcttct 510

Qy    927 ttgctggaactgtcattacgaccatagggtatgggaatattgctccgagcactgaaggag 986
          | ||  | || ||  |  | |||| ||| |||||  | |  |  ||     | || ||||
Db    511 tcgccagcaccgtgctctccaccacaggttatggccacaccgtgcccttgtcagatggag 570

Qy    987 gcaaaatcttttgtattttatatgccatctttggaattccactctttggtttcttattgg 1046
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Db    571 gtaaggccttctgcatcatctactccgtcattggcattcccttcaccctcctgttcctga 630

Qy   1047 ctggaattggagaccaacttggaaccatctttgggaaaagcattgcaagagtggagaagg 1106
          | |    ||  | ||| |     ||| |    |  |   |||   |     |  |
Db    631 cgg---ctgtggtccagcgcatcaccgtgcacgtcacccgcaggccggtcctctacttcc 687

Qy   1107 tctttcgaaaaaagcaagtgagtcagaccaagatccgggtcatctcaaccatcctgttca 1166
           | | ||             |  |||     |  |  |||    |     ||||
Db    688 acatccgctggggcttctccaagcaggtggtggccatcgtccatgccgtgctccttgggt 747

Qy   1167 tcttggccggctgcattgtgtttgtgacgatccctgctgtcatctttaagtacatcgagg 1226
          |  |  | |  | |    | ||  | |      | |||||| |||           || |
Db    748 ttgtcactgtgtcctgcttcttcttcatcccggccgctgtcttctcagtcctggaggatg 807

Qy   1227 gctggacggccttggagtccatttactttgtggtggtcactctgaccacggtgggctttg 1286
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Db    808 actggaacttcctggaatccttttatttttgttttatttccctgagcaccattggcctgg 867

Qy   1287 gtgattttgtggcaggggggaaacgctggcatcaattatcgggagtggtataagcccctag 1346
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Db    868 gggattatgtgcctggggaaggctacaatcaaaaattcagagagctctataagattggga 927

Qy   1347 tgtggttttggatccttgttggcctt 1372
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Db    928 tcacgtgttacctgctacttggcctt 953


RESULT   6
US-09-144-914-3
; Sequence 3, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
;  APPLICANT: Duprat, Fabrice
;  APPLICANT: Lesage, Florian
;  APPLICANT: Fink, Michel
;  APPLICANT: Lazdunski, Michel
;  TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
;  TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
;  FILE REFERENCE: 989.6705CIP
;  CURRENT APPLICATION NUMBER: US/09/144,914
;  CURRENT FILING DATE: 1998-09-01
;  EARLIER APPLICATION NUMBER: 08/749,816
;  EARLIER FILING DATE: 1996-11-15
;  EARLIER APPLICATION NUMBER: 60/095,234
;  EARLIER FILING DATE: 1998-08-04
;  EARLIER APPLICATION NUMBER: FR 96/01565
;  EARLIER FILING DATE: 1996-02-08
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 2514
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (126)..(1307)
;   FEATURE:
;   OTHER INFORMATION: TASK
US-09-144-914-3


  Query Match             3.8%;  Score 78.2;  DB 4;  Length 2514;
  Best Local Similarity   49.2%;  Pred. No. 6e-12;
  Matches  334;  Conservative    0;  Mismatches  323;  Indels   22;  Gaps    4;

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Db    341 caaggccggcgtgcagtggcgcttccgccggctccttctacttcgccatcaccgtcatcac 400

Qy    946 gaccatagggtatgggaatattgctccgagcactgaaggaggcaaaatcttttgtatttt 1005
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Db    401 caccatcggctacgggcacgcggcacccagcacggatggcggcaaggtgttctgcatgtt 460

Qy   1006 atatgccatctttggaattccactctttggtttcttattggctggaattggagaccaact 1065
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Db    461 ctacgcgctgctgggcatcccgctcacgctcgtcatgttccagagcctgggcgagcgcat 520

Qy   1066 tggaaccatctttgggaaaagcattgcaagagtggagaaggtctttcgaaaaaagcaagt 1125
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Db    521 caacaccttggtgaggtacctgctgcaccgcgccaagaaggggctgggca---------t 571

Qy   1126 gagtcagaccaagatccgggtcatctcaaccatcctgttcatcttggccggctgcattgt 1185
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Db    572 gcggcgcgccgacgtgtccatggccaacatggtgctcatcggcttcttctcgtgcatcag 631

Qy   1186 gtttgtgacgatccctgctgtcatctttaagtacatcgagggctggacggccttggagtc 1245
             ||   |||   || | |  |||     ||  ||||  ||||||   |||  || |
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Qy   1423 gtccaaaaagacaaaagaagaggtgggtgaaatcaaggcccatgcg----gcagagtgga 1478
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Qy   1479 aggccaatgtcacggctgagttccgggagacacggcgaaggctcagcgtggagatccacg 1538
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Db    926 cgggcaggcgggcggcggcggagggggtggcagcgcgcacactacggacaccgcctcatc 985

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RESULT 7
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F1s

US-08-232-463-14

Query Match 3.6%; Score 74.8; DB 1; Length 7218;
Best Local Similarity 5.4%; Pred. No. 9.6e-11;
Matches 22; Conservative 236; Mismatches 148; Indels 0; Gaps 0;

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Qy     75 aggctgcgcagcccctaacctgccggcaccgcttttgggaagcagcttggctcttccatc 134
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Db   1081 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1140

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Db   1141 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1200

Qy    195 cccacggggccgcggccggccaccccctggccggtgcaaacacccaagccctctccagtt 254
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Db   1201 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1260

Qy    255 ctccccccaagctaatattttcccacctgtctttttctggggttcctccacgagccagtcc 314
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Db   1321 YYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY 1380

Qy    375 tgaggactttattattatttgggttcttttcatttcttccccttct 420
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RESULT 8
US-08-332-312-1
; Sequence 1, Application US/08332312
; Patent No. 5559026
; GENERAL INFORMATION:
; APPLICANT: Price, Laura A.
; APPLICANT: Pausch, Mark H.
; TITLE OF INVENTION: Functional Expression of a Drosphila
; TITLE OF INVENTION: Melanagaster Putative Potassium Channel in Yeast
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: US
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/332,312
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Harrington, James J.
; REGISTRATION NUMBER: P-38,711
; REFERENCE/DOCKET NUMBER: 32,421
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3246
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2441 base pairs
; TYPE: nucleic acid

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;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  190..2043
US-08-332-312-1


  Query Match             2.6%;  Score 53.2;  DB 1;  Length 2441;
  Best Local Similarity   56.2%;  Pred. No. 5.7e-05;
  Matches  100;  Conservative    0;  Mismatches   78;  Indels    0;  Gaps    0;

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Db    517 AATATATCGCCAACCACCTTCGCCGGACGGATGATCATGATCGCGTATTCGGTGATTGGC 576

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RESULT   9
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
;  GENERAL INFORMATION:
;    APPLICANT:  DORNER, F.
;    APPLICANT:  SCHEIFLINGER, F.
;    APPLICANT:  FALKNER, F. G.
;    TITLE OF INVENTION:  RECOMBINANT FOWLPOX VIRUS
;    NUMBER OF SEQUENCES:  52
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/232,463
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,313
;      FILING DATE:
;      APPLICATION NUMBER:  EP 91 114 300.6
;      FILING DATE:  26-AUG-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  30472/114 IMMU
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7218 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      CLONE:  pTZgpt-Fls
US-08-232-463-14


  Query Match             2.5%;  Score 51.4;  DB 1;  Length 7218;
  Best Local Similarity   2.0%;  Pred. No. 0.00033;
  Matches    7;  Conservative  210;  Mismatches  136;  Indels    0;  Gaps    0;

Qy   1709 aacaacctgcgcctgaaggggccggagcagctgaacaagcatgggcagggtgcgtccgag 1768
          || ||  ||   | :::::::  :::: ::  ::: ::: : ::: :::: : :   :::
Db   1447 AAGAATTTGGTACRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1388

Qy   1769 gacaacatcatcaacaagttcgggtccacctccagactcaccaagaggaaaaacaaggac 1828
          :: :: :  :  :: :::   :::   :     :::   :  :::::::::::: :::::
Db   1387 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1328

Qy   1829 ctcaaaaagaccttgcccgaggacgttcagaaaatctacaagaccttccggaattactcc 1888
             :::::::    :   ::::: :   :::::::   : ::::      ::::  :
Db   1327 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1268

Qy   1889 ctggacgaggagaagaaagaggaggaaacggaaaaagatgtgtaactcagacaactccagc 1948
             ::: :::::::::::::::::::::: :::::::: : : ::   ::: ::    ::
Db   1267 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1208

Qy   1949 acagccatgctgacggactgtatccagcagcacgctgagttggagaacggaatgataccc 2008
          : ::  : :  :: :::  : :   :: :: : :  :::  :::::: :::: :: :
Db   1207 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1148

Qy   2009 acggacaccaaagaccgggagccggagaacaactcattacttgaagacagaaa 2061
          : ::: :  :::::  :::::  :::::: ::   :  :   ::::: :::::
Db   1147 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1095


RESULT  10
US-09-007-005-17/c
; Sequence 17, Application US/09007005B
; Patent No. 6258558
; GENERAL INFORMATION:
;  APPLICANT: Szostak, Jack W.
;  APPLICANT: Roberts, Richard W.
;  APPLICANT: Liu, Rihe
;  TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
;  TITLE OF INVENTION: FUSIONS
;  FILE REFERENCE: 00786/350003
;  CURRENT APPLICATION NUMBER: US/09/007,005B
;  CURRENT FILING DATE: 1998-01-14
;  EARLIER APPLICATION NUMBER: 60/035,963
;  EARLIER FILING DATE: 1997-01-27
;  EARLIER APPLICATION NUMBER: 60/064,491
;  EARLIER FILING DATE: 1997-11-06
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 289
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Translation template
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(289)
;   OTHER INFORMATION: n = A,T,C or G
US-09-007-005-17


  Query Match             2.4%;  Score 49;  DB 4;  Length 289;
  Best Local Similarity   6.9%;  Pred. No. 0.00026;
  Matches   16;  Conservative  109;  Mismatches  108;  Indels    0;  Gaps    0;

Qy     55 tctccgtagccccagccttcaggctgcgcagcccctaacctgccggcaccgctttttggga 114
          :|: : :|  : :|  :|:   |:|: :|  :|:|  ::: :  :: :  :: :  :
Db    257 YCYGYCYAYAYGYAYGYTYTYAYCYGYCYAYGYCYTYGYSYNYNYSYNYNYSYNYNYSYN 198

Qy    115 agcagcttggctcttccatctccccaagccttcctctccatcctttcatccacccctcgc 174
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           :   :  :: : ::: : ::: :  :: : ::: : : : : : : : : : ::
Db    197 YNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYN 138

Qy    175 cgatcttacttttttcttttacccacggggccgcggccggccacccccctggccggtgcaaa 234
          :   : : : : : : : : ::: :  :  : ::  :  :: : :::   ::  : :
Db    137 YNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYN 78

Qy    235 cacccaagccctctccagttctcccccaagctaatattttcccacctgtcttt 287
          : :::   ::: : ::  : : : : :  |:| |:|:|:|: : : : : :|:
Db     77 YNYSYNYNYSYNYNYSYNYNYCYAYTYTYGYTYAYAYTYTYGYTYAYAYAYTY 25


RESULT  11
US-09-244-796-17/c
; Sequence 17, Application US/09244796
; Patent No. 6281344
; GENERAL INFORMATION:
;  APPLICANT: Szostak, Jack W.
;  APPLICANT: Roberts, Richard W.
;  APPLICANT: Liu, Rihe
;  TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
;  TITLE OF INVENTION: FUSIONS
;  FILE REFERENCE: 00786/350007
;  CURRENT APPLICATION NUMBER: US/09/244,796
;  CURRENT FILING DATE: 1999-02-05
;  EARLIER APPLICATION NUMBER: 60/035,963
;  EARLIER FILING DATE: 1997-01-27
;  EARLIER APPLICATION NUMBER: 60/064,491
;  EARLIER FILING DATE: 1997-11-06
;  EARLIER APPLICATION NUMBER: 09/007,005
;  EARLIER FILING DATE: 1998-01-14
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;   LENGTH: 289
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Translation template
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(289)
;   OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17


  Query Match             2.4%;  Score 49;  DB 4;  Length 289;
  Best Local Similarity   6.9%;  Pred. No. 0.00026;
  Matches   16;  Conservative  109;  Mismatches  108;  Indels    0;  Gaps    0;

Qy     55 tctccgtagccccagccttcaggctgcgcagcccctaacctgccggcaccgcttttggga 114
          :|: : :|  : :|  :|:    |:|: :|  :|:|  ::: :  :: :  :: :  :
Db    257 YCYGYCYAYAYGYAYGYTYTYAYCYGYCYAYGYCYTYGYSYNYNYSYNYNYSYNYNYSYN 198

Qy    115 agcagcttggctcttccatctccccaagccttcctctccatcctttcatccacccctcgc 174
          :   :  :: : ::: : ::: :  :: : ::: : : : : : : : : : ::
Db    197 YNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYN 138

Qy    175 cgatcttacttttttcttttacccacggggccgcggccggccacccccctggccggtgcaaa 234
          :   : : : : : : : : ::: :  :  : ::  :  :: : :::   ::  : :
Db    137 YNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYNYNYSYN 78

Qy    235 cacccaagccctctccagttctcccccaagctaatattttcccacctgtcttt 287
          : :::   ::: : ::  : : : : :  |:| |:|:|:|: : : : : :|:
Db     77 YNYSYNYNYSYNYNYSYNYNYCYAYTYTYGYTYAYAYTYTYGYTYAYAYAYTY 25


RESULT  12
US-08-332-312-3
; Sequence 3, Application US/08332312
; Patent No. 5559026
;  GENERAL INFORMATION:
;    APPLICANT:  Price, Laura A.
;    APPLICANT:  Pausch, Mark H.
;    TITLE OF INVENTION:  Functional Expression of a Drosphila
;    TITLE OF INVENTION:  Melanagaster Putative Potassium Channel in Yeast
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  American Cyanamid Company
;      STREET:  One Cyanamid Plaza
;      CITY:  Wayne
;      STATE:  New Jersey
;      COUNTRY:  US
;      ZIP:  07470-8426
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/332,312
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Harrington, James J.
;      REGISTRATION NUMBER:  P-38,711
;      REFERENCE/DOCKET NUMBER:  32,421
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-831-3246
;      TELEFAX:  201-831-3305
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1011 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1008
US-08-332-312-3


  Query Match             2.2%;  Score 44.8;  DB 1;  Length 1011;
  Best Local Similarity   62.5%;  Pred. No. 0.0077;
  Matches   70;  Conservative    0;  Mismatches   42;  Indels    0;  Gaps    0;

Qy    918 ccttttttctttgctggaactgtcattacgaccatagggtatgggaatattgctccgagca 977
          || |||||||||| | ||| ||| | || ||||| || || || |||   | |||    |
Db     98 CCATTTTCTTTGCCGTAACCGTCGTCACTACCATCGGATACGGTAATCCAGTTCCAGTGA 157

Qy    978 ctgaaggaggcaaaatcttttgtattttatatgccatctttggaattccact 1029
          |  |    ||    || |  ||||| || |   || |  ||||||| || ||
Db    158 CAAACATTGGACGGATATGGTGTATATTGTTCTCCTTGCTTGGAATACCTCT 209


RESULT  13
US-08-928-361B-2
; Sequence 2, Application US/08928361B
; Patent No. 6071518
;  GENERAL INFORMATION:
;    APPLICANT:  Petersen, Carolyn
;    TITLE OF INVENTION:  PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
;    TITLE OF INVENTION:  THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
;    TITLE OF INVENTION:  FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
;    TITLE OF INVENTION:  SPECIES INFECTIONS
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PETERS, VERNY, JONES & BIKSA
;      STREET:  385 Sherman Avenue, Suite 6
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306-1840
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/928,361B
;       FILING DATE:  12-SEP-1997
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 60/026,062
;       FILING DATE:  13-SEP-1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Verny, Hana
;       REGISTRATION NUMBER:  30,518
;       REFERENCE/DOCKET NUMBER:  480.76-1(HV)
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  650-324-1677
;       TELEFAX:  650-324-1678
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  5511 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-928-361B-2


  Query Match             2.1%;  Score 43.8;  DB 3;  Length 5511;
  Best Local Similarity   44.6%;  Pred. No. 0.038;
  Matches  171;  Conservative    0;  Mismatches  212;  Indels    0;  Gaps    0;

Qy   1659 acaccggccgcttcaaggcctcatcccaggagagcatcaacaaccggcccaacaacctgc 1718
          ||| |  |  || | |   ||  | | | || | || |||||||     |||||||
Db    934 ACAACAACAACTACTACTACTACTACGACAACAACAACAACAACGACAACAACAACA 993

Qy   1719 gcctgaaggggccggagcagctgaacaagcatgggcagggtgcgtccgaggacaacatca 1778
          |    |        | ||    || |  |       |       | | | ||||||| ||
Db    994 ACTACTACAACTACTACCACTACTACTACGACAACAACAACTACTACTACGACAACAACA 1053

Qy   1779 tcaacaagttcgggtccacctccagactcaccaagaggaaaaacaaggacctcaaaaaga 1838
          ||||||  | |   | |  || ||  | || |||    ||  || |  ||  |||  | |
Db   1054 ACAACAACTACTACTACTACTACAACCACAACAACTACAACCACGACAACTACAACCACA 1113

Qy   1839 ccttgcccgaggacgttcagaaaatctacaagaccttccggaattactccctggacgagg 1898
          |     | |  | |     || | | |||| | |  |   || |||| |    || |
Db   1114 ACCACAACTACCAAGAAACCAACAACAACAACAACAACAACAACTACTACTACTACAACA 1173

Qy   1899 agaagaaagaggaggaaacggaaaagatgtgtaactcagacaactccagcacagccatgc 1958
          | || ||  |  |  |     |  |   |   |||  || ||| |  |     |   |
Db   1174 ACAACAACAACAACTACTACTACTACTACTACTACTACTACTACTACTACTACTACC 1233

Qy   1959 tgacggactgtatccagcagcacgctgagttggagaacggaatgatacccacggacacca 2018
            |   ||   | |||  | |||    |    || | |   |  |    ||   ||| ||
Db   1234 ACAACAACCACAACCACAACCACAACTACCAAGAAACCAACAACAACAACAACAACAACA 1293

Qy   2019 aagaccgggagccggagaacaac 2041
          |  ||    |     | ||| ||
Db   1294 ACAACAACTACTACTACAACCAC 1316


RESULT  14
US-08-928-361B-1
; Sequence 1, Application US/08928361B
; Patent No. 6071518
;  GENERAL INFORMATION:
;    APPLICANT:  Petersen, Carolyn
;    TITLE OF INVENTION:  PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
;    TITLE OF INVENTION:  THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
;    TITLE OF INVENTION:  FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
;    TITLE OF INVENTION:  SPECIES INFECTIONS
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PETERS, VERNY, JONES & BIKSA
;      STREET:  385 Sherman Avenue, Suite 6
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94306-1840
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/928,361B
;      FILING DATE:  12-SEP-1997
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 60/026,062
;      FILING DATE:  13-SEP-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Verny, Hana
;      REGISTRATION NUMBER:  30,518
;      REFERENCE/DOCKET NUMBER:  480.76-1(HV)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-324-1677
;      TELEFAX:  650-324-1678
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7334 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-928-361B-1


  Query Match             2.1%;  Score 43.8;  DB 3;  Length 7334;
  Best Local Similarity   44.6%;  Pred. No. 0.045;
  Matches  171;  Conservative    0;  Mismatches  212;  Indels    0;  Gaps    0;

Qy   1659 acaccggccgcttcaaggcctcatcccaggagagcatcaacaaccggcccaacaacctgc 1718
          ||| |  |  || | |   ||  | | | || | || |||||||     |||||||
Db   2602 ACAACAACAACTACTACTACTACTACGACAACAACAACAACAACGACAACAACAACA 2661

Qy   1719 gcctgaaggggccggagcagctgaacaagcatgggcagggtgcgtccgaggacaacatca 1778
          |    |        | ||    || |  |       |       | | | ||||||| ||
Db   2662 ACTACTACAACTACTACCACTACTACTACGACAACAACAACTACTACTACGACAACAACA 2721

Qy   1779 tcaacaagttcgggtccacctccagactcaccaagaggaaaaacaaggacctcaaaaaga 1838
          ||||||  | |   | |  || ||  | || |||    ||  || |  ||  |||  | |
Db   2722 ACAACAACTACTACTACTACAACCACAACAACTACAACCACGACAACTACAACCACA 2781

Qy   1839 ccttgcccgaggacgttcagaaaatctacaagaccttccggaattactccctggacgagg 1898
          |     | |  | |     || | | |||| | |  |   || |||| |    || |
Db   2782 ACCACAACTACCAAGAAACCAACAACAACAACAACAACAACAACTACTACTACTACAACA 2841

Qy   1899 agaagaaagaggaggaaacggaaaagatgtgtaactcagacaactccagcacagccatgc 1958
          | || ||  |  |  |     |  |   |   |||  || ||| |  |     |   |
Db   2842 ACAACAACAACAACTACTACTACTACTACTACTACTACTACTACTACTACTACTACC 2901

Qy   1959 tgacggactgtatccagcagcacgctgagttggagaacggaatgatacccacggacacca 2018
            |   ||   | |||  | |||    |    || | |   |  |    ||   ||| ||
Db   2902 ACAACAACCACAACCACAACCACAACTACCAAGAAACCAACAACAACAACAACAACAACA 2961

Qy   2019 aagaccgggagccggagaacaac 2041
          |  ||    |     | ||| ||
Db   2962 ACAACAACTACTACTACAACCAC 2984


RESULT  15
US-08-804-227C-1
; Sequence 1, Application US/08804227C
; Patent No. 5876991
;  GENERAL INFORMATION:
;    APPLICANT:  DeHoff, Bradley S.
```

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;    APPLICANT:  Kuhstoss, Stuart A.
;    APPLICANT:  Rosteck, Paul R., Jr.
;    APPLICANT:  Sutton, Kimberly L.
;    TITLE OF INVENTION:  POLYKETIDE SYNTHASE GENES
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  THOMAS G. PLANT  1501
;      STREET:  LILLY CORPORATE CENTER
;      CITY:  INDIANAPOLIS
;      STATE:  IN
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  ASCI(DOS) Text only
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/804,227C
;      FILING DATE:  February 21, 1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plant, Thomas, G.
;      REGISTRATION NUMBER:  35,784
;      REFERENCE/DOCKET NUMBER:  X-8231
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  317-276-2459
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  43280 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  816..14234
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  14351..19945
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  20010..31199
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  31232..36067
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  36249..41774
US-08-804-227C-1


  Query Match             2.1%;  Score 42.6;  DB 2;  Length 43280;
  Best Local Similarity   48.5%;  Pred. No. 0.26;
  Matches  117;  Conservative    0;  Mismatches  124;  Indels    0;  Gaps    0;

Qy   1528 ggagatccacgataagctgcagcgggcggccaccatccgcagcatggagcgccggcggct 1587
          || ||||  ||  ||    | |  |  |||| |  |  | |    ||  |   |  |||
Db  25322 GGTGATCTCCGCCAACGGCCGGTCGAGGGCCTTCGCCGCCGGTGCCGACGGTGTGGCGCT 25381

Qy   1588 gggcctggaccagcgggcccactcactggacatgctgtcccccgagaagcgctctgtctt 1647
           |||  || |  | | | ||      ||||   ||||||   ||   |||||   | |
Db  25382 CGGCGAGGGCGTGGGCGTCCTGCTGGTGGAGCGGCTGTCGGACGCCGAGCGCAACGGCCA 25441

Qy   1648 tgctgccctggacaccggccgcttcaaggcctcatcccaggagagcatcaacaaccggcc 1707
          | | |  ||||     | ||||  |  |||      ||||||  ||  |  |||| |||
Db  25442 TCCGGTGCTGGCGGTGGTCCGCGGCTCGGCGGTCAACCAGGACGGCGCCTCCAACGGGCT 25501

Qy   1708 caacaacctgcgcctgaaggggccggagcagctgaacaagcatgggcagggtgcgtccga 1767
           |    |    |  |       | | ||| | ||| |  ||| | || ||  |   |||
Db  25502 GACGGCGCCCAACGGGCCCTCCCAGCAGCGGGTGATCCGGCAGGCGCTGGCGGACGCCGG 25561

Qy   1768 g 1768
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          |
Db  25562 G 25562


Search completed: September 21, 2002, 08:33:07
Job time: 10018 sec
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: September 21, 2002, 05:43:19 ; Search time 2190.54 Seconds
(without alignments)
12723.444 Million cell updates/sec

Title: US-09-729-920-1
Perfect score: 2065
Sequence: 1 ggacactgacatggactgaa.....tacttgaagacagaaactaa 2065

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	696.4	33.7	960	10	BI669964	BI669964 603294474
	2	634.8	30.7	1360	11	AK019376	AK019376 Mus muscu
	3	516.2	25.0	680	9	BB128596	BB128596 BB128596
	4	476.8	23.1	552	9	AW784769	AW784769 115015 MA
	5	475.4	23.0	636	9	BB659274	BB659274 BB659274
	6	453	21.9	1103	11	AK006295	AK006295 Mus muscu
	7	386.8	18.7	645	9	BB622028	BB622028 BB622028
	8	358.4	17.4	680	9	BB649994	BB649994 BB649994
	9	193.8	9.4	401	9	AA464375	AA464375 zx81d11.r
c	10	173.4	8.4	689	9	BB641499	BB641499 BB641499
c	11	171.6	8.3	1089	12	CNS044VV	AL274612 Tetraodon
	12	164.2	8.0	283	9	BB304952	BB304952 BB304952
	13	163.2	7.9	723	12	CNS055BR	AL321840 Tetraodon
	14	156.8	7.6	923	10	BF569718	BF569718 602186245
	15	150	7.3	593	9	AI073392	AI073392 ov46a03.x
	16	147.8	7.2	922	10	BI758226	BI758226 603029871
	17	137.4	6.7	519	10	BF191397	BF191397 238973 MA
	18	136	6.6	521	10	BF193457	BF193457 245052 MA
	19	136	6.6	531	10	BF191393	BF191393 238967 MA
c	20	134	6.5	590	10	BE981482	BE981482 UI-M-CG0p
	21	134	6.5	598	12	AZ406369	AZ406369 1M0175O04
	22	134	6.5	609	9	AU177116	AU177116 AU177116
c	23	132.4	6.4	593	10	BE981393	BE981393 UI-M-CG0p
c	24	128	6.2	376	9	BE185995	BE185995 IL5-HT073
	25	127.8	6.2	648	10	BM426281	BM426281 pgf2n.pk0
	26	123.4	6.0	612	12	B65883	B65883 CIT-HSP-202
	27	122.2	5.9	622	10	BF739947	BF739947 7o41d02.x
	28	117.8	5.7	469	10	BF565047	BF565047 UI-R-BO1-
	29	114.4	5.5	2128	11	AK014626	AK014626 Mus muscu
	30	113.8	5.5	665	9	BB628772	BB628772 BB628772
	31	112.8	5.5	484	12	AQ078760	AQ078760 CIT-HSP-2
	32	106.2	5.1	903	12	CNS02U9Q	AL214199 Tetraodon
	33	104	5.0	676	9	AI956397	AI956397 ul74g06.y
	34	101.2	4.9	433	9	AW141778	AW141778 EST291867
	35	100.4	4.9	586	10	BE680493	BE680493 df81b01.y
c	36	99.6	4.8	892	9	AL537214	AL537214 AL537214
	37	99.4	4.8	839	10	BI656440	BI656440 603285768
	38	97.8	4.7	563	10	BI066457	BI066457 pgf1n.pk0
	39	97.6	4.7	248	9	AV040667	AV040667 AV040667
	40	93.8	4.5	436	9	AI816233	AI816233 au45h10.y
	41	93.6	4.5	242	9	AV042781	AV042781 AV042781
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	43	91.6	4.4	882	10	BG919070	BG919070 602817932
	44	91.2	4.4	655	10	BG017630	BG017630 dab09b01.
	45	90.8	4.4	857	10	BI157909	BI157909 602923078

ALIGNMENTS

RESULT 1
BI669964
LOCUS BI669964 960 bp mRNA linear EST 12-SEP-2001
DEFINITION 603294474F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5313738 5', mRNA sequence.
ACCESSION BI669964
VERSION BI669964.1 GI:15584197
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 960)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11795 row: c column: 19
High quality sequence stop: 736.
FEATURES Location/Qualifiers
source 1. .960
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5313738"
/clone_lib="NIH_MGC_96"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and

normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT 252 a 249 c 278 g 181 t
ORIGIN

Query Match 33.7%; Score 696.4; DB 10; Length 960;
Best Local Similarity 97.2%; Pred. No. 6.1e-153;
Matches 762; Conservative 0; Mismatches 16; Indels 6; Gaps 5;

```
Qy   1280 ggctttggtgattttgtggcaggggaaacgctggcatcaattatcgggagtggtataag 1339
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4 GGCTTTGGTGATTTTGTGGCAGGGGGAAACGCTGGCATCAATTATCGGGAGTGGTATAAG 63

Qy   1340 cccctagtgtggttttggatccttgttggccttgcctactttgcagctgtcctcagtatg 1399
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Qy   1400 atcggagattggctacgggttctgtccaaaaagacaaaagaagaggtgggtgaaatcaag 1459
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Qy   1460 gcccatgcggcagagtggaaggccaatgtcacggctgagttccgggagacacggcgaagg 1519
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Db    183 GCCCATGCGGCAGAGTGGAAGGCCAATGTCACGGCTGAGTTCCGGGAGACACGGCGAAGG 242

Qy   1520 ctcagcgtggagatccacgataagctgcagcgggcggccaccatccgcagcatggagcgc 1579
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Qy   1580 cggcggctgggcctggaccagcgggcccactcactggacatgctgtcccccgagaagcgc 1639
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Qy   1640 tctgtctttgctgccctggacaccggccgcttcaaggcctcatcccaggagagcatcaac 1699
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Qy   1700 aaccggcccaacaacctgcgcctgaaggggccggagcagctgaacaagcatgggcagggt 1759
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Qy   1760 gcgtccgaggacaacatcatcaacaagttcgggtccacctccagactcaccaagaggaaa 1819
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Qy   1820 aacaaggacctcaaaaagaccttgcccgaggacgttcagaaaatctacaagaccttccgg 1879
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Qy   1880 aattactccctggacgaggagaagaaagaggaggaaacggaa-aagatgtgtaactcaga 1938
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Qy   1939 caactccagcacagccatgct--gacggactgtatccagcagcacgctgagttggagaac 1996
          |||||||||||||||||||     | ||||||||||||||||||||||||||||||||||
Db    663 CAACTCCAGCACAGCCATGCTTGACGGAACTGTATCCAGCAGCACGCTGAGTTGGAGAAC 722

Qy   1997 ggaatgatacccacggacaccaaagaccgggagccggagaacaactcattacttgaagac 2056
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Db    723 GGAATGATTCCCACGGGACCCCAAGACC-GGAGCCGGAGAAC-ACTCCTTACTTGGAGAC 780

Qy   2057 agaa 2060
            ||
Db    781 GAAA 784
```

RESULT 2
AK019376
LOCUS AK019376 1360 bp mRNA linear HTC 19-JAN-2002
DEFINITION Mus musculus 12 days embryo head cDNA, RIKEN full-length enriched library, clone:3010005K24:homolog to POTASSIUM CHANNEL SUBFAMILY K MEMBER 10 (OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TREK-2) (TREK-2 K+ CHANNEL SUBUNIT), full insert sequence.
ACCESSION AK019376
VERSION AK019376.1 GI:12859546
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (strain:C57BL/6J) 12 days embryo head cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:3010005K24.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (sites)
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2 (sites)
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3 (sites)
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4 (sites)
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5 (bases 1 to 1360)
AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F., Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (18-AUG-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

```
          Division of Experimental Animal Research in Riken contributed to
          prepare mouse tissues. First strand cDNA was primed with a primer
          [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
          prepared by using trehalose thermo-activated reverse transcriptase
          and subsequently enriched for full-length by cap-trapper. cDNA went
          through one round of normalization to Rot = 10.0 and subtraction to
          Rot = 50.0. Second strand cDNA was prepared with the primer adapter
          of sequence [5'
          GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved
          with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
          Host: SOLR.
FEATURES             Location/Qualifiers
     source          1. .1360
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                     /strain="C57BL/6J"
                     /db_xref="MGD:MGI:1911272"
                     /db_xref="taxon:10090"
                     /clone="3010005K24"
                     /tissue_type="head"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="12 days embryo"
     CDS             507. .1232
                     /note="data source:SPTR, source key:Q9JIS4, evidence:ISS
                     homolog to POTASSIUM CHANNEL SUBFAMILY K MEMBER 10
                     (OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TREK-2)
                     (TREK-2 K+ CHANNEL SUBUNIT)
                     putative"
                     /codon_start=1
                     /protein_id="BAB31686.1"
                     /db_xref="GI:12859547"
                     /translation="MKFPIETPRKQVNWDPKVAVPAAAPPVCQPKSATNGHHPVPRLS
                     ISSRATVVARMEGASQGGLQTVMKWKTVVAIFVVVVVYLVTGGLVFRALEQPFESSQK
                     NTIALEKAEFLRDHICVSPQELETLIQHALDADNAGVSPVGNSSNSSSHWDLGSAFFF
                     AGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVE
                     KVFRAHGCFVCTHIFVPGIHGSH"
     polyA_signal    1341. .1346
                     /note="putative"
     polyA_site      1360
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BASE COUNT      297 a    356 c    350 g    357 t
ORIGIN


  Query Match           30.7%;  Score 634.8;  DB 11;  Length 1360;
  Best Local Similarity   79.8%;  Pred. No. 2e-138;
  Matches  878;  Conservative    0;  Mismatches  172;  Indels   50;  Gaps    9;

Qy      35 gagtgacactgcagtgggcttctccgtagccccagccttcaggctgcgcagcccctaacc 94
           ||| ||| |||| ||||||||| |    ||| | |||    |||||| ||||| |  | |
Db     113 GAGGGACGCTGCGGTGGGCTTCACTCCGGCCTCCGCCCGGCGGCTGCTCAGCCTCGCATC 172

Qy      95 tgccggcaccgcttttgg-gaagcagcttggctcttccatctccccaagccttcctctcc 153
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Db     173 TGCCTACCGCGCTTTTGCAGAAGCAGCCCGGCTCTTTGATCCTC---------------- 216

Qy     154 atccttttcatccacccctcgccgatcttactttttctttttacccacg-gggccgcggccg 212
           ||    |  ||  |     |||||||||||||||||| ||||||  |||| || || |
Db     217 -TCGGAACCACCCTCAGCATCCGATCTTACTTTTTCTTTCACCCACAAGGGCAGCAGCTG 275

Qy     213 gccacccccc-tggccggtgcaaacacccaa-----gccctctccagttctcccccaagct 266
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Db     276 GCCACCCCCTTAACCGGTGCAAACACCCAACCAAGCCAGTGCTCGGTGCTTTCCTCTGCT 335

Qy     267 aatattttcccacctgtctttttctggggttcctccacgagccagtccaaggctcccccca 326
           | |||||||||  ||    |||    |||    | ||||||||| | ||  ||||| |||
Db     336 AGTATTTTCCCCGCTTGTCTTTCTCTGGGGCTCCCCACGAGCCACTTCAGTGCTCCTCCA 395

Qy     327 tcctcggaaattgttttgttggactgctaaaccgaggcg-tgtaaagcttgaggact--- 382
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Db     396 TCCTCACAAATTGTTCCGTTGGTCTGTTTAACCGACGAGTTGTAAATCTTGAAGACTTTA 455

Qy     383 ttattattatttgggttcttttcatttcttccccttctgggcaacgaagcaatgaaattt 442
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Qy     443 ccaatcgagacgccaagaaaacaggtgaactgggatcctaaagtggccgttcccgcagca 502
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Db     516 CCAATCGAGACGCCAAGAAAGCAGGTGAACTGGGATCCTAAAGTGGCCGTGCCTGCAGCA 575

Qy     503 g---caccggtgtgccagcccaagagcgccactaacgggcaacccccggctccggctccg 559
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Db     576 GCCCCACCAGTGTGCCAGCCCAAGAGTGCCACTAACGGGCATCACCCTG----------- 624

Qy     560 actccaactccgcgcctgtccatttcctcccgagccacagtggtagccaggatggaaggc 619
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Db     625 -------TTCCTCGACTCTCCATTTCCTCTCGAGCCACGGTGGTAGCCAGGATGGAAGGC 677

Qy     620 acctcccaaggggcttgcagaccgtcatgaagtggaagacggtggttgccatctttgtg 679
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Db     678 GCCTCCCAGGGAGGCCTGCAAACAGTTATGAAGTGGAAAACAGTGGTTGCCATCTTCGTG 737

Qy     680 gttgtggtggtctaccttgtcactggcggtcttgtcttccgggcattggagcagccccttt 739
           || || |||||||||| |||||||| || |||||||||||||| ||||| ||||||||
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Qy     740 gagagcagccagaagaataccatcgccttggagaaggcggaattcctgcgggatcatgtc 799
           |||||||| |||||||| || ||||||||||||||||| |||||| || | |||||  ||
Db     798 GAGAGCAGTCAGAAGAACACAATCGCCTTGGAGAAGGCAGAATTCTTGAGAGATCACATC 857

Qy     800 tgtgtgagcccccaggagctggagacgttgatccagcatgctcttgatgctgacaatgcg 859
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Db     858 TGTGTGAGTCCCCAGGAACTAGAGACACTGATTCAGCATGCACTCGATGCTGATAACGCG 917

Qy     860 ggagtcagtccaataggaaactcttccaacaacagcagccactgggacctcggcagtgcc 919
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Qy     920 ttttttctttgctggaactgtcattacgaccatagggtatgggaatattgctccgagcact 979
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Db     978 TTCTTCTTTGCTGGGACAGTCATCACAACCATAGGGTATGGGAATATTGCTCCGAGCACT 1037

Qy     980 gaaggaggcaaaatcttttgtattttatatgccatctttggaattccactctttggtttc 1039
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Db    1038 GAAGGAGGCAAAATCTTTTGTATTTTATATGCCATCTTTGGGATCCCGCTTTTTGGTTTC 1097

Qy    1040 ttattggctggaattggagaccaacttggaaccatctttgggaaaagcattgcaagagtg 1099
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Qy    1100 gagaaggtctttcgaaaaaa 1119
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Db    1158 GAAAAGGTTTTTCGAGCACA 1177


RESULT   3
BB128596
LOCUS       BB128596                680 bp    mRNA    linear   EST 31-AUG-2001
DEFINITION  BB128596 RIKEN full-length enriched, 16 days neonate cerebellum Mus
            musculus cDNA clone 9630032C21 3', mRNA sequence.
ACCESSION   BB128596
VERSION     BB128596.2  GI:15408288
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 680)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.
            , Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
            ,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
            Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
            ,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
            Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
  JOURNAL   Unpublished (2001)
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COMMENT     On Jun 28, 2000 this sequence version replaced gi:8782968.
            Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
            ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. . 10 (10), 1617-1630 (2000)
             wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
            ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
            Hayashizaki,Y.
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
            10 (11), 1757-1771 (2000)
             Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
            ,Y. and Hayashizaki,Y.
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
             Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A., Aizawa
            ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K., Arakawa,T.,
            Ishii,Y. and Hayashizaki,Y.
             Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
            Func. Genomics 2 pre, L72-L86 (2001)
             Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
FEATURES              Location/Qualifiers
     source           1. .680
                      /organism="Mus musculus"
                      /db_xref="taxon:10090"
                      /clone="9630032C21"
                      /clone_lib="RIKEN full-length enriched, 16 days neonate
                      cerebellum"
                      /tissue_type="cerebellum"
                      /dev_stage="16 days neonate"
                      /lab_host="DH10B"
                      /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                      prepared and sequenced in Mouse Genome Encyclopedia
                      Project of Genome Exploration Research Group in Riken
                      Genomic Sciences Center and Genome Science Laboratory in
                      RIKEN. Division of Experimental Animal Research in Riken
                      contributed to prepare mouse tissues. 1st strand cDNA was
                      primed with a primer [5'
                      GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                      prepared by using trehalose thermo-activated reverse
                      transcriptase and subsequently enriched for full-length by
                      cap-trapper. cDNA went through one round of normalization
                      to Rot = 20.0 and subtraction to Rot = 370.0. Second
                      strand cDNA was prepared with the primer adapter of
                      sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC
                      3']. cDNA was cleaved with XhoI and BamHI. Vector: a
                      modified pBluescript KS(+) after bulk excision from Lambda
                      FLC I."
BASE COUNT      165 a    164 c    194 g    157 t
ORIGIN
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  Query Match             25.0%;  Score 516.2;  DB 9;  Length 680;
  Best Local Similarity   86.0%;  Pred. No. 1.3e-110;
  Matches  584;  Conservative    0;  Mismatches   93;  Indels    2;  Gaps    1;

Qy   1135 caagatccgggtcatctcaaccatcctgttcatcttggccggctgcattgtgtttgtgac 1194
          |||||| |||||||| || || ||  | |||  || ||  ||  |   |  | |||||||
Db      4 CAAGATTCGGGTCATTTCCACGATTTTTTTCTACTAGGTGGG--GGCATTGGGTTGTGAC 61

Qy   1195 gatccctgctgtcatctttaagtacatcgagggctggacggccttggagtccatttactt 1254
           |||||||||||||||||||| |||||  |||| ||| | ||| ||||||||||||||||
Db     62 CATCCCTGCTGTCATCTTTAAATACATGAAGGGGTGGGCCGCCCTGGAGTCCATTTACTT 121

Qy   1255 tgtggtggtcactctgaccacggtgggctttggtgattttgtggcaggggggaaacgctgg 1314
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Qy   1315 catcaattatcgggagtggtataagcccctagtgtggttttggatccttgttggccttgc 1374
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Db    182 CATCAATTTCCGAGAGTGGTACAAGCCGCTGGTGTGGTTTTGGATCCTTGTTGGCCTTGC 241

Qy   1375 ctactttgcagctgtcctcagtatgatcggagattggctacgggttctgtccaaaaagac 1434
          ||||||||||||||||||||||||||||||||| ||||| |||||| | ||||||||||
Db    242 CTACTTTGCAGCTGTCCTCAGTATGATCGGAGACTGGCTGCGGGTTTTATCCAAAAAGAC 301

Qy   1435 aaaagaagaggtgggtgaaatcaaggcccatgcggcagagtggaaggccaatgtcacggc 1494
          |||||||||||| ||||| ||||| ||||| || || |||||||||| |||||||| ||
Db    302 AAAAGAAGAGGTTGGTGAGATCAAAGCCCACGCAGCTGAGTGGAAGGCTAATGTCACTGC 361

Qy   1495 tgagttccgggagacacggcgaaggctcagcgtggagatccacgataagctgcagcgggc 1554
          ||||||||||||||  |  |  |||||||||| |||||||| || |||||||| |||||
Db    362 TGAGTTCCGGGAGACGAGAAGGCGGCTCAGCGTTGAGATCCATGACAAGCTGCAACGGGC 421

Qy   1555 ggccaccatccgcagcatggagcgccggcggctgggcctggaccagcgggcccactcact 1614
          |||||  ||||| || |||||||||||| |||||||| |||||||| ||||||||||||
Db    422 AGCCACTATCCGAAGTATGGAGCGCCGGAGGCTGGGCTTGGACCAGAGGGCCCACTCACT 481

Qy   1615 ggacatgctgtcccccgagaagcgctctgtctttgctgccctggacaccggccgcttcaa 1674
          |||||||| ||||| |||||||| |||||||||| |||||||||| ||||| |||||
Db    482 GGACATGCTATCCCCTGAGAAGCGTTCTGTCTTTGCAGCCCTGGACACAGGCCGTTTCAA 541

Qy   1675 ggcctcatcccaggagagcatcaacaaccggcccaacaacctgcgcctgaaggggccgga 1734
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Qy   1735 gcagctgaacaagcatgggcagggtgcgtccgaggacaacatcatcaacaagttcgggtc 1794
           ||||| | ||| |||||||||| || |  |||||||||||||||||||||||| |||||
Db    602 ACAGCTTACCAAACATGGGCAGGGCGCTTTTGAGGACAACATCATCAACAAGTTTGGGTC 661

Qy   1795 cacctccagactcaccaag 1813
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Db    662 CACCTCCAAACTCACAAAG 680
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RESULT   4
AW784769
LOCUS       AW784769                552 bp    mRNA    linear   EST 09-JUL-2000
DEFINITION  115015 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   AW784769
VERSION     AW784769.1  GI:7841545
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 552)
  AUTHORS   Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
            and Keele,J.W.
  TITLE     Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
```

```
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 43  row: M  column: 16
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .552
                     /organism="Sus scrofa"
                     /db_xref="taxon:9823"
                     /clone_lib="MARC 1PIG"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
                     Library made from pooled tissue from day 11, 13, 15, 20,
                     and 30 embryos."
BASE COUNT      144 a    162 c    176 g     70 t
ORIGIN


  Query Match             23.1%;  Score 476.8;  DB 9;  Length 552;
  Best Local Similarity   91.5%;  Pred. No. 2.2e-101;
  Matches  505;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy   1399 gatcggagattggctacgggttctgtccaaaaagacaaaagaagaggtgggtgaaatcaa 1458
          ||||||||||||||||||||||||| ||||||||||||| |||||||||||||| |||||
Db      1 GATCGGAGATTGGCTACGGGTTCTATCCAAAAAGACAAAGGAAGAGGTGGGTGAGATCAA 60

Qy   1459 ggcccatgcggcagagtggaaggccaatgtcacggctgagttccgggagacacggcgaag 1518
          |||||| ||||| |||||||||||||| || ||||| ||||| |||||||| |||||  |
Db     61 GGCCCACGCGGCCGAGTGGAAGGCCAACGTGACGGCCGAGTTTCGGGAGACGCGGCGGCG 120

Qy   1519 gctcagcgtggagatccacgataagctgcagcgggcggccaccatccgcagcatggagcg 1578
          ||| |||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db    121 GCTGAGCGTGGAGATCCACGACAAGCTGCAGCGGGCGGCCACCATCCGCAGCATGGAGCG 180

Qy   1579 ccggcggctgggcctggaccagcgggcccactcactggacatgctgtcccccgagaagcg 1638
          |||||| |||||||||||||| |||||||||| || |||||||| ||||| ||||||||
Db    181 CCGGCGCCTGGGCCTGGACCAGAGGGCCCACTCGCTCGACATGCTCTCCCCGGAGAAGCG 240

Qy   1639 ctctgtctttgctgccctggacaccggccgcttcaaggcctcatcccaggagagcatcaa 1698
          ||| ||||| || || |||||| ||||||||||||||||||| ||||||||||||||||
Db    241 CTCCGTCTTCGCCGCGCTGGACGCCGGCCGCTTCAAGGCCTCGTCCCAGGAGAGCATCAA 300

Qy   1699 caaccggcccaacaacctgcgcctgaaggggccggagcagctgaacaagcatgggcaggg 1758
          |||||||||||||||||||||||| ||||| | |||||||||||||| || ||||||||
Db    301 CAACCGGCCCAACAACCTGCGCCTGCAGGGGTCCGAGCAGCTGAACAAACACGGGCAGGG 360

Qy   1759 tgcgtccgaggacaacatcatcaacaagttcgggtccacctccagactcaccaagaggaa 1818
            || || ||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db    361 GGCCTCGGAGGACAACATCATCAACAAGTTCGGGTCCACCTCCAGGCTCACCAAGAGGAA 420

Qy   1819 aaacaaggacctcaaaaagaccttgcccgaggacgttcagaaaatctacaagaccttccg 1878
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Db    421 AAACAAGGACCTCAAAAAGACCTTGCCCGAGGACGTGCAAAAGATCTACAAGACTTTCCG 480

Qy   1879 gaattactccctggacgaggagaagaaagaggaggaaacggaaaagatgtgtaactcaga 1938
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Qy   1939 caactccagcac 1950
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Db    541 TCACTCGAGCAC 552


RESULT   5
BB659274
LOCUS       BB659274                636 bp    mRNA    linear   EST 26-OCT-2001
DEFINITION  BB659274 RIKEN full-length enriched, 13 days embryo heart Mus
            musculus cDNA clone D330028P16 5', mRNA sequence.

ACCESSION   BB659274
VERSION     BB659274.1  GI:16493096
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 636)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.
            , Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
            ,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
            Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
            ,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
            Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
            ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. . 10 (10), 1617-1630 (2000)
             wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
            ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
            Hayashizaki,Y.
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
            10 (11), 1757-1771 (2000)
             Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
            ,Y. and Hayashizaki,Y.
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
             Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
            ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
            Hayashizaki,Y.
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
             e mouse tissues.
FEATURES             Location/Qualifiers
     source          1. .636
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                     heart"
                     /tissue_type="heart"
                     /dev_stage="13 days embryo"
                     /lab_host="DH10B"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAGCGGCCGCAACTCGAGTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. Second strand cDNA was prepared with the
                     primer adapter of sequence [5'
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GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."
BASE COUNT 196 a 151 c 164 g 123 t 2 others
ORIGIN

Query Match 23.0%; Score 475.4; DB 9; Length 636;
Best Local Similarity 88.5%; Pred. No. 4.9e-101;
Matches 515; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

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Db     62 CTGCAACGGGCAGCCACTATCCGAAGTATGGAGCGCCGGAGGCTGGGCTTGGACCAGAGG 121

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Db    122 GCCCACTCACTGGACATGCTATCCCCTGAGAAGCGTTCTGTCTTTGCAGCCCTGGACACA 181

Qy   1664 ggccgcttcaaggcctcatcccaggagagcatcaacaaccggcccaacaacctgcgcctg 1723
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Db    182 GGCCGTTTCAAGGCCTCATCGCAGGAGAGTATCAACAACAGACCCAACAACCTACGCCTT 241

Qy   1724 aaggggccggagcagctgaacaagcatgggcagggtgcgtccgaggacaacatcatcaac 1783
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Db    242 AAGGGGCCAGAACAGCTTACCAAACATGGGCAGGGCGCTTCTGAGGACAACATCATCAAC 301

Qy   1784 aagttcgggtccacctccagactcaccaagaggaaaaacaaggacctcaaaaagaccttg 1843
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Db    302 AAGTTTGGGTCCACCTCCAAACTCACAAAGAGGAAAAACAAAGATCTCAAAAAGACCTTA 361

Qy   1844 cccgaggacgttcagaaaatctacaagaccttccggaattactccctggacgaggagaag 1903
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Db    362 CCCGAGGATGTTCAGAAAATCTACAGAACCTTCCGGAATTACTCTCTGGATGAAGAGAAG 421

Qy   1904 aaagaggaggaaacggaaaagatgtgtaactcagacaactccagcacagccatgctgacg 1963
          |||||||| || || |||||||||||||||| |||||||||||||||||||||||||||
Db    422 AAAGAGGACGAGACAGAAAAGATGTGTAACTCCGACAACTCCAGCACAGCCATGCTGACA 481

Qy   1964 gactgtatccagcagcacgctgagttggagaacggaatgatacccacggacaccaaagac 2023
          || ||||| |||||||| |||||| |||||||||||||| ||||||||||||||||||||
Db    482 GAGTGTATACAGCAGCAAGCTGAGATGGAGAACGGAATGGTACCCACGGACACCAAAGAC 541

Qy   2024 cgggagccggagaacaactcattacttgaagacagaaactaa 2065
          | || || ||||||||| || |||||||||||||| |||||
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```

RESULT 6
AK006295
LOCUS AK006295 1103 bp mRNA linear HTC 19-JAN-2002
DEFINITION Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:1700024D23:homolog to POTASSIUM CHANNEL SUBFAMILY K MEMBER 10 (OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TREK-2) (TREK-2 K+ CHANNEL SUBUNIT), full insert sequence.
ACCESSION AK006295
VERSION AK006295.1 GI:12839321
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (strain:C57BL/6J) adult male testis cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:1700024D23.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (sites)
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2 (sites)
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3 (sites)
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4 (sites)
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5 (bases 1 to 1103)
AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F., Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence[5' GAGAGAGAGAGCGGCCGCAATTAATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI. Host: SOLR.
FEATURES Location/Qualifiers
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/db_xref="MGD:MGI:1905038"
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/clone="1700024D23"
/sex="male"
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                     (TREK-2 K+ CHANNEL SUBUNIT)
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BASE COUNT      277 a    276 c    279 g    271 t
ORIGIN


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  Matches  534;  Conservative    0;  Mismatches   70;  Indels   19;  Gaps    2;

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Db    390 TGCAGCAGCCCCACCAGTGTGCCAGCCCAAGAGTGCCACTAACGGGCATCACCCTGTTCC 449

Qy    553 ggctccgactccaactccgcgcctgtccatttcctcccgagccacagtggtagccaggat 612
                          || || |||||||||||| |||||||| ||||||||||||||
Db    450 T------------------CGACTCTCCATTTCCTCTCGAGCCACGGTGGTAGCCAGGAT 491

Qy    613 ggaaggcacctcccaaggggcttgcagaccgtcatgaagtggaagacggtggttgccat 672
          ||||||| ||||||| || ||| |||| || || |||||||||||| || ||||||||||||
Db    492 GGAAGGCGCCTCCCAGGGAGGCCTGCAAACAGTTATGAAGTGGAAAACAGTGGTTGCCAT 551

Qy    673 ctttgtggttgtggtggtctaccttgtcactggcggtcttgtcttccgggcattggagca 732
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Db    552 CTTCGTGGTGGTCGTGGTCTACCTCGTCACTGGTGGCCTTGTCTTCCGGGCCTTGGAACA 611

Qy    733 gccctttgagagcagccagaagaataccatcgccttggagaaggcggaattcctgcggga 792
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Db    612 GCCCTTCGAGAGCAGTCAGAAGAACACAATCGCCTTGGAGAAGGCAGAATTCTTGAGAGA 671

Qy    793 tcatgtctgtgtgagcccccaggagctggagacgttgatccagcatgctcttgatgctga 852
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Db    672 TCACATCTGTGTGAGTCCCCAGGAACTAGAGACACTGATTCAGCATGCACTCGATGCTGA 731

Qy    853 caatgcgggagtcagtccaataggaaactcttccaacaacagcagccactgggacctcgg 912
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Qy    913 cagtgccttttttctttgctggaactgtcattacgaccatagggtatgggaatattgctcc 972
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Qy    973 gagcactgaaggaggcaaaatcttttgtattttatatgccatctttggaattccac-tct 1031
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Db    852 GAGCACTGAAGGAGGCAAAATCTTTTGTATTTTATATGCCATCTTTGGGATCCCGCTTTT 911

Qy   1032 ttggtttcttattggctggaattggagaccaacttggaaccatctttgggaaaagcattg 1091
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Db    912 TTGGTTTCTTATTGGCTGGAATTGGAGACCAACTTGGAACCATCTTTGGCAAAAGCATTG 971

Qy   1092 caagagtggagaaggtctttcga 1114
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Db    972 CAAGAGTGGAAAAGGTTTTTCGA 994


RESULT   7
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LOCUS       BB622028                645 bp    mRNA    linear   EST 26-OCT-2001
DEFINITION  BB622028 RIKEN full-length enriched, adult male medulla oblongata
            Mus musculus cDNA clone 6330442J09 5', mRNA sequence.
ACCESSION   BB622028
VERSION     BB622028.1  GI:16461217
KEYWORDS    EST.
SOURCE      house mouse.
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 645)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.
            , Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
            ,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
            Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki
            ,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H.,
            Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
            ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
             Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new
            genes. Genome Res. . 10 (10), 1617-1630 (2000)
             wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
            Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
            ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
            Hayashizaki,Y.
             RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer. Genome Res. .
            10 (11), 1757-1771 (2000)
             Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara
            ,Y. and Hayashizaki,Y.
             Computer-based methods for the mouse full-length cDNA
            encyclopedia: real-time sequence clustering for construction of a
            nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
             Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
            ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
            Hayashizaki,Y.
             Computational Analysis of Full-Length Mouse cDNAs Compared with
            Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
             Please visit our web site (http://genome.gsc.riken.go.jp) for
            further details.
             e mouse tissues.
FEATURES             Location/Qualifiers
     source          1. .645
                     /organism="Mus musculus"
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                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
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transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI"

BASE COUNT 141 a 179 c 173 g 147 t 5 others
ORIGIN

Query Match 18.7%; Score 386.8; DB 9; Length 645;
Best Local Similarity 83.1%; Pred. No. 3.4e-80;
Matches 481; Conservative 0; Mismatches 77; Indels 21; Gaps 3;

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Qy    553 ggctccgactccaactccgcgcctgtccatttcctcccgagccacagtggtagccaggat 612
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Db    188 GGAAGGCGCCTCCCAGGGAGGCCTGCAAACAGTTATGAAGTGGAAAACAGTGGTTGCCAT 247

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Qy    793 tcatgtctgtgtgagcccccaggagctggagacgttgatccagcatgctcttgatgctga 852
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Db    367 TCACATCTGTGTGAGTCCCCAGGAACTAGAGACACTGATTCAGCATGCACTCGATGCTGA 426

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RESULT 8
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LOCUS BB649994 680 bp mRNA linear EST 26-OCT-2001
DEFINITION BB649994 RIKEN full-length enriched, 0 day neonate cerebellum Mus musculus cDNA clone C230015H11 5', mRNA sequence.
ACCESSION BB649994
VERSION BB649994.1 GI:16484249
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 680)
AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
TITLE RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
JOURNAL Unpublished (2001)
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
e mouse tissues.

FEATURES Location/Qualifiers
source 1. .680
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="C230015H11"
/clone_lib="RIKEN full-length enriched, 0 day neonate cerebellum"
/tissue_type="cerebellum"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 479.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

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ORIGIN

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Qy    535 cgggcaacccccggctccggctccgactccaactccgcgcctgtccatttcctcccgagc 594
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Qy    655 gaagacggtggttgccatctttgtggttgtggtggtctaccttgtcactggcggtcttgt 714
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Qy    715 cttccgggcattggagcagccctttgagagcagccagaagaataccatcgccttggagaa 774
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Qy    775 ggcggaattcctgcgggatcatgtctgtgtgagcccccaggagctggagacgttgatcca 834
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Qy    835 gcatgctcttgatgctgacaatgcgggagtcagtccaataggaaactcttccaacaacag 894
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Db    491 GCATGCACTCGATGCTGATAACGCGGGAGTCAGCCCAGTAGGAAACTCTTCC-ACAGCAG 549

Qy    895 cagccactgggacctcggcagtgccttttttctttgctggaactgtcattacgaccatagg 954
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Qy   1015 ctttggaattcc 1026
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AA464375
LOCUS       AA464375                401 bp    mRNA    linear   EST 10-JUN-1997
DEFINITION  zx81d11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
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            sequence.
ACCESSION   AA464375
VERSION     AA464375.1  GI:2189259
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 401)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
            Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B.
            , Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie
            ,T., Waterston,R. and Wilson,R.
  TITLE     WashU-Merck EST Project 1997
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 315.
FEATURES             Location/Qualifiers
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                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. "
BASE COUNT      111 a     83 c     86 g    121 t
ORIGIN


  Query Match             9.4%;  Score 193.8;  DB 9;  Length 401;
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Qy    859 gggagtcagtccaataggaaactcttccaacaacagcagccactgggacctcggcagtgc 918
            ||  | |  ||  || ||||| | |||||  | | ||| ||||||||  | || ||| |
Db     62 AGGGATTATACCGTTA-GAAACACCTCCAATCAAATCAGTCACTGGGATTTGGGAAGTTC 120

Qy    919 ctttttctttgctggaactgtcattacgaccatagggtatgggaatattgctccgagcac 978
          ||| |||||||||| ||||| ||||| |||||||| | ||| || ||  | ||  ||||
Db    121 CTTCTTCTTTGCTGGCACTGTTATTACAACCATAGGATTTGGAAACATCTCACCACGCAC 180

Qy    979 tgaaggaggcaaaatcttttgtattttatatgccatctttggaattccactctttggtttt 1038
          ||||| |||||||| || |||||  | ||||||  |  | ||||||||  ||||||||||
Db    181 AGAAGGCGGCAAAATATTCTGTATCATCTATGCCTTACTGGGAATTCCCCTCTTTGGTTT 240

Qy   1039 cttattggctggaattggagaccaacttggaaccatctttgggaaaagcattgcaagagt 1098
            | |||||||| ||||||| || || || ||||| ||||| ||| | ||||| | |||
Db    241 TCTCTTGGCTGGAGTTGGAGATCAGCTAGGCACCATATTTGGAAAAGGAATTGCCAAAGT 300

Qy   1099 ggagaaggtctttcgaaaaaagcaagtgagtcagaccaagatccgggtcatctcaaccat 1158
          |||  |    |||   ||   | | || ||||||||||||||  ||  |||||||||  ||
Db    301 GGAAGATACGTTTATTAAGTGGAATGTTAGTCAGACCAAGATTCGCATCATCTCAACAAT 360

Qy   1159 cctgttcatcttggccggctgcattgtgtttgtgacgatcc 1199
          | | || ||  |    |||||  |  | ||||||  |  | |
Db    361 CATATTTATACTATTTGGCTGTGTACTCTTTGTGGCTCTGC 401


RESULT  10
BB641499/c
LOCUS       BB641499                689 bp    mRNA    linear   EST 26-OCT-2001
DEFINITION  BB641499 RIKEN full-length enriched, 10 days neonate cortex Mus
            musculus cDNA clone A830028F14 5', mRNA sequence.
ACCESSION   BB641499
VERSION     BB641499.1  GI:16476623
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 689)
  AUTHORS   Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.
            , Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda
            ,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M.,
```

Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki ,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.

TITLE RIKEN Mouse ESTs (Arakawa,T., et al. 2001)

JOURNAL Unpublished (2001)

COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh ,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura ,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara ,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa ,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
e mouse tissues.

FEATURES Location/Qualifiers
source 1. .689
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A830028F14"
/clone_lib="RIKEN full-length enriched, 10 days neonate cortex"
/tissue_type="cortex"
/dev_stage="10 days neonate"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 20.0 and subtraction to Rot = 459.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

BASE COUNT 182 a 182 c 203 g 121 t 1 others

ORIGIN

Query Match 8.4%; Score 173.4; DB 9; Length 689;
Best Local Similarity 71.9%; Pred. No. 5e-30;

Matches 333; Conservative 0; Mismatches 101; Indels 29; Gaps 7;

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Qy     35 gagtgacactgcagtgggcttctccgtagccccagccttcaggctgcgcagcccctaacc 94
          ||| ||| |||| ||||||||| |    ||| | |||    |||||| ||||| |  | |
Db    540 GAGGGACGCTGCGGTGGGCTTCACTCCGGCCTCCGCCCGGCGGCTGCTCAGCCTCGCATC 481

Qy     95 tgccggcaccgcttttgg-gaagcagcttggctcttccatctccccaagccttcctctcc 153
          ||||  |  |||||||| ||||||| |||||||  |||  |
Db    480 TGCCTACCGCGCTTTTGCAGAAGCAGCCCGGCTCTTTGATCCTC---------------- 435

Qy    154 atcctttcatccacccctcgccgatcttacttttttcttttacccacg-gggccgcggccg 212
           ||    |  ||  |     ||||||||||||||||||| ||||||  |||| || || |
Db    436 -TCGGAACCACCCTCAGCATCCGATCTTACTTTTTCTTTCACCCACAAGGGCAGCAGCTG 378

Qy    213 gccacccccc-tggccggtgcaaacacccaa-----gccctctccagttctcccccaagct 266
          |||||||||  |  ||||||||||||||||      |  |   | || ||  ||   |||
Db    377 GCCACCCCCTTAACCGGTGCAAACACCCAACCAAGCCAGTGCTCGGTGCTTTCCTCTGCT 318

Qy    267 aatattttcccacctgtctttttctggggttcctccacgagccagtccaaggctccccca 326
          | |||||||||  ||   |||   |||   | ||||||||||  | ||  ||||| |||
Db    317 AGTATTTTCCCCGCTTGTCTTTCTCTGGGGCTCCCCACGAGCCACTTCAGTGCTCCTCCA 258

Qy    327 tcctcggaaattgttttgttggactgctaaaccgaggcg-tgtaaagcttgaggact--- 382
          |||||  ||||||||  ||||| ||| | |||||| | | |||||| ||||| ||||
Db    257 TCCTCACAAATTGTTCCGTTGGTCTGTTTAACCGACGAGTTGTAAATCTTGAAGACTTTA 198

Qy    383 ttattattatttgggttcttttcatttcttccccttctgggcaacgaagcaatgaaattt 442
          |||||||||||| | |||||||||||| ||||| | |||||||| ||||||||||||
Db    197 TTATTATTATTTTGATTCTTTTCATTTCATCCCCCTGTGGGCAACGGAGCAATGAAATTT 138

Qy    443 ccaatcgagacgccaagaaaacaggtgaactgggatcctaaag 485
          |||||||||||||||||||| ||||||||||||||||||||||
Db    137 CCAATCGAGACGCCAAGAAAGCAGGTGAACTGGGATCCTAAAG 95
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RESULT 11
CNS044VV/c
LOCUS CNS044VV 1089 bp DNA linear GSS 18-MAY-2000
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 082I20 of library G from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION AL274612
VERSION AL274612.1 GI:8008812
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis.
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.
REFERENCE 1 (bases 1 to 1089)
AUTHORS Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
TITLE Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1089)
AUTHORS Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
TITLE Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1089)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
FEATURES Location/Qualifiers

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     source          1. .1089
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                     /db_xref="taxon:99883"
                     /clone="082I20"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0BG082BE10LP1~end : T7"
BASE COUNT      233 a    292 c    270 g    287 t      7 others
ORIGIN


  Query Match             8.3%;  Score 171.6;  DB 12;  Length 1089;
  Best Local Similarity   73.0%;  Pred. No. 1.5e-29;
  Matches  219;  Conservative    1;  Mismatches   80;  Indels    0;  Gaps    0;

Qy    1463 catgcggcagagtggaaggccaatgtcacggctgagttccgggagacacggcgaaggctc 1522
           || || || || ||||| ||||| ||   ||| ||| | ||||| || |||||  | ||
Db     546 CACGCAGCTGAATGGAAAGCCAACGTGCGGGCAGAGCTGCGGGAAACGCGGCGGCGTCTG 487

Qy    1523 agcgtggagatccacgataagctgcagcgggcggccaccatccgcagcatggagcgccgg 1582
           ||||| ||| ||| ||| ||||| ||||| || || |||||||||||||||| |||||
Db     486 AGCGTCGAGGTCCTCGACAAGCTCCAGCGAGCCGCGACCATCCGCAGCATGGAACGCCGT 427

Qy    1583 cggctgggcctggaccagcgggcccactcactggacatgctgtcccccgagaagcgctct 1642
           | |||||||||||| |||||||| || || |||:|||||| |||| ||||||||  ||
Db     426 CAGCTGGGCCTGGAGCAGCGGGCTCATTCCCTGKACATGCTCTCCCCGGAGAAGCGGGCT 367

Qy    1643 gtctttgctgccctggacaccggccgcttcaaggcctcatcccaggagagcatcaacaac 1702
           | ||||||   || ||  |   |||||||||| |||| |||||||||||||  ||| |
Db     366 CTGTTTGCTAGTCTCGATGCTAACCGCTTCAAGACCTCCTCCCAGGAGAGCATTGACACC 307

Qy    1703 cggcccaacaacctgcgcctgaaggggccggagcagctgaacaagcatgggcagggtgcg 1762
             ||  |||||||||   |||||||| |     ||    |||| ||   |  | | | |
Db     306 AAGCTTAACAACCTGAAGCTGAAGGGCGCCTGCGAGTCATACAACCAGCAGGGGAGCGAG 247


RESULT  12
BB304952
LOCUS       BB304952                283 bp    mRNA    linear   EST 10-JUL-2000
DEFINITION  BB304952 RIKEN full-length enriched, adult male corpora
            quadrigemina Mus musculus cDNA clone B230115M11 3', mRNA sequence.
ACCESSION   BB304952
VERSION     BB304952.1  GI:9005657
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 283)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
            ,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.
            , Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.
            , Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
            ,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.
            , Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya
            ,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.
            , Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino
            ,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
            ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
            ,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .283
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /clone="B230115M11"
                     /clone_lib="RIKEN full-length enriched, adult male corpora
                     quadrigemina"
                     /sex="male"
                     /tissue_type="corpora quadrigemina"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 20.0 and subtraction to Rot = 459.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC
                     3']. cDNA was cleaved with XhoI and BamHI. Vector: a
                     modified pBluescript KS(+) after bulk excision from Lambda
                     FLC I."
BASE COUNT       95 a     72 c     58 g     58 t
ORIGIN


  Query Match             8.0%;  Score 164.2;  DB 9;  Length 283;
  Best Local Similarity   79.3%;  Pred. No. 5.8e-28;
  Matches  207;  Conservative    0;  Mismatches   53;  Indels    1;  Gaps    1;

Qy    1806 tcaccaagaggaaaaacaaggacctcaaaaagaccttgcccgaggacgttcagaaaatct 1865
           || || ||| |    |||   |  ||  | ||||| | ||||   |  ||||| |||| |
Db       1 TCTCCGAGATGCTCCACATACATTTCCGACAGACCCTACCCGTCCATCTTCAGGAAATTT 60

Qy    1866 acaagaccttccggaattactccctggacgaggagaag-aaagaggaggaaacggaaaag 1924
           || | ||||||| ||||||||| ||||| || ||||||  ||||||| || || ||| ||
Db      61 ACCAAACCTTCCTGAATTACTCTCTGGATGAAGAGAAGCCAAGAGGACGAGACAGAATAG 120

Qy    1925 atgtgtaactcagacaactccagcacagccatgctgacggactgtatccagcagcacgct 1984
           |||||||||| |||||||||||||| |||| ||||| || ||||| || || |  |||
Db     121 ATGTGTAACTCCGACAACTCCAGCACACCCATCCTGACAGAGTGTATACACCACCTAGCT 180

Qy    1985 gagttggagaacggaatgatacccacggacaccaaagaccgggagccggagaacaactca 2044
           ||| |||||||||| ||| ||||||||||||||||||| || || ||||||||| ||
Db     181 GAGATGGAGAACGGTATGGTACCCACGGACACCAAAGACCAGGGGCTGGAGAACAATTCT 240

Qy    2045 ttacttgaagacagaaactaa 2065
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Db     241 TTACTTGAAGACAGAAACTAA 261


RESULT  13
CNS055BR
LOCUS       CNS055BR                723 bp    DNA     linear   GSS 26-JUL-2000
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DEFINITION  Tetraodon nigroviridis genome survey sequence T7 end of clone
            029K21 of library A from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL321840
VERSION     AL321840.1  GI:9554724
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis.
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 723)
  AUTHORS   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
  JOURNAL   Nat. Genet. 25 (2), 235-238 (2000)
  MEDLINE   20296633
REFERENCE   2  (bases 1 to 723)
  AUTHORS   Crollius,H.R., Jaillon,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C.,
            Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W.,
            Bernot,A. and Weissenbach,J.
  TITLE     Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish tetraodon nigroviridis
  JOURNAL   Genome Res. 10 (7), 939-949 (2000)
  MEDLINE   20359837
REFERENCE   3  (bases 1 to 723)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .723
                     /organism="Tetraodon nigroviridis"
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                     /clone="029K21"
                     /clone_lib="A"
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ORIGIN
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  Query Match             7.9%;  Score 163.2;  DB 12;  Length 723;
  Best Local Similarity   70.9%;  Pred. No. 1.3e-27;
  Matches  227;  Conservative    0;  Mismatches   92;  Indels    1;  Gaps    1;

Qy   1444 ggtgggtgaaatcaaggcccatgcggcagagtggaaggc-caatgtcacggctgagttcc 1502
          | |||       || || || || || || ||||| || ||| ||   ||| ||| | |
Db     14 GTTGGAGAGNNNTAAAGCTCACGCAGCTGAATGGAAAGCGCAACGTGCGGGCAGAGCTGC 73

Qy   1503 gggagacacggcgaaggctcagcgtggagatccacgataagctgcagcgggcggccacca 1562
          |||| || |||||  | || ||||| ||| ||| ||| ||||  ||||| || || ||||
Db     74 GGGAAACGCGGCGGCGTCTGAGCGTCGAGGTCCTCGACAAGCNCCAGCGAGCCGCGACCA 133

Qy   1563 tccgcagcatggagcgccggcggctgggcctggaccagcgggcccactcactggacatgc 1622
          |||||||||||| ||||| | |||||||||||| |||||||| || || ||||||||||
Db    134 TCCGCAGCATGGAACGCCGTCAGCTGGGCCTGGAGCAGCGGGCTCATTCCCTGGACATGC 193

Qy   1623 tgtcccccgagaagcgctctgtctttgctgccctggacaccggccgcttcaaggcctcat 1682
          | ||||| |||||||| || | |||||||   || ||  |   |||||||||| |||| |
Db    194 TCTCCCCGGAGAAGCGGGCTCTGTTTGCTAGTCTCGATGCTAACCGCTTCAAGACCTCCT 253

Qy   1683 cccaggagagcatcaacaaccggcccaacaacctgcgcctgaaggggccggagcagctga 1742
          ||||||||||||  ||| |  ||  |||||||||   |||||||| |      ||
Db    254 CCCAGGAGAGCATTGACACCAAGCTTAACAACCTGAAGCTGAAGGGCGCCTGCGAGTCAT 313

Qy   1743 acaagcatgggcagggtgcg 1762
          |||| ||   |  | | | |
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Db    314 ACAACCAGCAGGGGAGCGAG 333
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RESULT  14
BF569718
LOCUS       BF569718                923 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  602186245F1 NIH_MGC_45 Homo sapiens cDNA clone IMAGE:4310506 5',
            mRNA sequence.
ACCESSION   BF569718
VERSION     BF569718.1  GI:11643098
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 923)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Linehan
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1185  row: j  column: 11
            High quality sequence stop: 734.
FEATURES             Location/Qualifiers
     source          1. .923
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4310506"
                     /clone_lib="NIH_MGC_45"
                     /tissue_type="renal carcinoma (ascites)"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: kidney; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life  Technologies). Note: this is a
                     NIH_MGC Library. |"
BASE COUNT      245 a    197 c    238 g    243 t
ORIGIN
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  Query Match             7.6%;  Score 156.8;  DB 10;  Length 923;
  Best Local Similarity   74.2%;  Pred. No. 4.4e-26;
  Matches  239;  Conservative    0;  Mismatches   77;  Indels    6;  Gaps    3;

Qy   1243 gtccatttactttgtggtggtcactctgaccacggtgggctttggtgattttgtggcagg 1302
          | ||||||| ||||||||  ||||||| || ||  |||   ||||||| |  || |||||
Db      1 GGCCATTTATTTTGTGGTTATCACTCTAACAACTATGG--ATTGGTGACTACGTTGCAGG 58

Qy   1303 gggaaacgctggcatcaattatcgggagtggtataagcccctagtgtggttttggatcct 1362
          |||  || |   ||  | |||| ||| |  |||||||  | |||||||| ||||||||
Db     59 TGGATCCGAT---ATTGAATATCTGGACTTCTATAAGCCTGTCGTGTGGTTCTGGATCCT 115

Qy   1363 tgttggccttgcctactttgcagctgtcctcagtatgatcggagattggctacgggttct 1422
          ||| || ||||| |||||||| |||||||| || ||||| ||||| ||||| || ||  |
Db    116 TGTAGGGCTTGCTTACTTTGCTGCTGTCCTGAGCATGATTGGAGA-TGGCTCCGAGTGAT 174

Qy   1423 gtccaaaaagacaaaagaagaggtgggtgaaatcaaggcccatgcggcagagtggaaggc 1482
          || |||||||||||||||||||||||||| ||  |||  || || || || |||||||  ||
Db    175 ATCTAAAAAGACAAAAGAAGAGGTGGGAGAGTTCAGAGCACACGCTGCTGAGTGGACAGC 234

Qy   1483 caatgtcacggctgagttccgggagacacggcgaaggctcagcgtggagatccacgataa 1542
          ||| ||||| || || |||   || ||  || |  | || || ||||||||  | || ||
Db    235 CAACGTCACAGCCGAATTCAAAGAAACCAGGAGGCGACTGAGTGTGGAGATTTATGACAA 294
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Qy   1543 gctgcagcgggcggccaccatc 1564
          | | ||||||||  || |||||
Db    295 GTTCCAGCGGGCCACCTCCATC 316


RESULT 15
AI073392
LOCUS       AI073392                593 bp    mRNA    linear   EST 27-AUG-1998
DEFINITION  ov46a03.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1640332
            3' similar to TR:P97438 P97438 TWIK-1 RELATED POTASSIUM CHANNEL,
            SUBFAMILY K, MEMBER 2 ;, mRNA sequence.
ACCESSION   AI073392
VERSION     AI073392.1  GI:3400036
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 593)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
            , Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1154   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 459.
FEATURES             Location/Qualifiers
     source          1. .593
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1640332"
                     /clone_lib="Soares_testis_NHT"
                     /sex="male"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from mRNA obtained from Clontech Laboratories
                     , Inc., and primed with  a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTT 3']. 
                     Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization to Cot5, and was
                     constructed  by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      162 a    110 c    138 g    183 t
ORIGIN


  Query Match             7.3%;  Score 150;  DB 9;  Length 593;
  Best Local Similarity   96.8%;  Pred. No. 1.5e-24;
  Matches  153;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy   1292 tttgtggcaggggaaacgctggcatcaattatcgggagtggtataagcccctagtgtgg 1351
           ||  |  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    393 TTGTTTTCAGGGGGAAACGCTGGCATCAATTATCGGGAGTGGTATAAGCCCCTAGTGTGG 452

Qy   1352 ttttggatccttgttggccttgcctactttgcagctgtcctcagtatgatcggagattgg 1411
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    453 TTTTGGATCCTTGTTGGCCTTGCCTACTTTGCAGCTGTCCTCAGTATGATCGGAGATTGG 512

Qy   1412 ctacgggttctgtccaaaaagacaaaagaagaggtggg 1449
           |||||||||||||||||||||||||||||||||| ||
Db    513 CTACGGGTTCTGTCCAAAAAGACAAAAGAAGAGGTAGG 550
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Search completed: September 21, 2002, 07:27:27
Job time: 6248 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: September 21, 2002, 08:33:09 ; Search time 64.01 Seconds
(without alignments)
942.245 Million cell updates/sec

Title: US-09-729-920-2
Perfect score: 2795
Sequence: 1 MKFPIETPRKQVNWDPKVAV.....IPTDTKDREPENNSLLEDRN 543

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1630	58.3	383	22	ABG02731	Novel human diagno
2	1412.5	50.5	557	22	ABG08305	Novel human diagno
3	1251.5	44.8	411	21	AAE10342	Murine TREK-1 pota
4	1248.5	44.7	411	20	AAY28497	Mouse h-TREK1 poly
5	1247.5	44.6	370	20	AAY30648	A mechanically sen
6	1243	44.5	411	21	AAE10341	Human TREK-1 potas
7	1242.5	44.5	411	20	AAY34133	Human potassium ch
8	1242.5	44.5	411	20	AAY28496	h-TREK1 polypeptid
9	1242.5	44.5	411	22	AAB50044	Human TREK. Homo
10	1218.5	43.6	426	22	AAU07618	Human potassium io
11	1218.5	43.6	426	22	AAU07622	Human potassium io
12	1214.5	43.5	426	22	AAU07623	Human potassium io
13	1210.5	43.3	426	22	AAU07624	Human potassium io
14	1210.5	43.3	426	22	AAU07625	Human potassium io
15	822.5	29.4	1314	22	AAU04571	Human G-protein co
16	812.5	29.1	393	21	AAY94425	Human h-TRAAK poly
17	812.5	29.1	393	21	AAY94426	Human h-TRAAK poly
18	812.5	29.1	393	22	AAG67777	Human mechanically
19	790	28.3	398	20	AAY30647	A mechanically sen
20	774	27.7	155	22	AAM24148	Human EST encoded
21	607.5	21.7	421	22	ABB12229	Human K channel TR
22	483.5	17.3	511	22	ABG26753	Novel human diagno
23	483	17.3	499	21	AAY90356	Human TWIK-2 prote
24	483	17.3	499	21	AAY79675	Human potassium ch
25	483	17.3	499	21	AAY94875	Human protein clon
26	483	17.3	499	22	AAE01026	Human TWIK-2 prote
27	447	16.0	107	20	AAY28498	Partial h-TREK1 po
28	403	14.4	336	18	AAW23397	TWIK-1 potassium c
29	403	14.4	336	21	AAY79673	Human potassium ch
30	400	14.3	781	22	ABG26754	Novel human diagno
31	396	14.2	332	21	AAY90354	Human TWIK-3 prote
32	396	14.2	332	22	AAE01027	Human TWIK-3 prote
33	361	12.9	361	22	AAB31805	Amino acid sequenc
34	352.5	12.6	405	21	AAY95230	Mouse potassium ch
35	352	12.6	400	22	AAE10679	Human TWIK-6 (G 16
36	349.5	12.5	394	21	AAE10343	Murine TASK potass
37	349.5	12.5	394	21	AAY79674	Human potassium ch
38	349.5	12.5	394	21	AAY87291	Human signal pepti
39	344	12.3	400	22	AAE10678	Human TWIK-6 (E 16
40	334	11.9	374	21	AAB18807	Amino acid sequenc
41	334	11.9	374	21	AAB18813	Protein encoded by
42	334	11.9	374	22	AAG63938	Amino acid sequenc
43	333.5	11.9	313	20	AAY34132	Human potassium ch
44	333.5	11.9	313	20	AAY25116	Human hTREK-1 prot
45	333.5	11.9	313	21	AAY90355	Human TWIK-4 prote

ALIGNMENTS

RESULT 1
ABG02731
ID ABG02731 standard; Protein; 383 AA.
XX
AC ABG02731;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #2722.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS66918.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess

```
PT   biodiversity  -
XX
PS   Claim 20; SEQ ID No 33090; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   383 AA;


  Query Match            58.3%;  Score 1630;  DB 22;  Length 383;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-139;
  Matches  317;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     227 RKKQVSQTKIRVISTILFILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGD 286
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67 rkkqvsqtkirvistilfilagcivfvtipavifkyiegwtalesiyfvvvtlttvgfgd 126

Qy     287 FVAGGNAGINYREWYKPLVWFWILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAA 346
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     127 fvaggnaginyrewykplvwfwilvglayfaavlsmigdwlrvlskktkeevgeikahaa 186

Qy     347 EWKANVTAEFRETRRRLSVEIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPEKRSVFA 406
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     187 ewkanvtaefretrrrlsveihdklqraatirsmerrrlgldqrahsldmlspekrsvfa 246

Qy     407 ALDTGRFKASSQESINNRPNNLRLKGPEQLNKHGQGASEDNIINKFGSTSRLTKRKNKDL 466
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     247 aldtgrfkassqesinnrpnnlrlkgpeqlnkhgqgasedniinkfgstsrltkrknkdl 306

Qy     467 KKTLPEDVQKIYKTFRNYSLDEEKKEEETEKMCNSDNSSTAMLTDCIQQHAELENGMIPT 526
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     307 kktlpedvqkiyktfrnyslddeekkeeetekmcnsdnsstamltdciqqhaelengmipt 366

Qy     527 DTKDREPENNSLLEDRN 543
           |||||||||||||||||
Db     367 dtkdrepennslledrn 383


RESULT   2
ABG08305
ID   ABG08305 standard; Protein; 557 AA.
XX
AC   ABG08305;
XX
DT   13-FEB-2002  (first entry)
XX
DE   Novel human diagnostic protein #8296.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS72492.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity  -
XX
PS   Claim 20; SEQ ID No 38664; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   557 AA;


  Query Match            50.5%;  Score 1412.5;  DB 22;  Length 557;
  Best Local Similarity  72.4%;  Pred. No. 2e-119;
  Matches  297;  Conservative    2;  Mismatches   18;  Indels   93;  Gaps    4;

Qy     227 RKKQVSQTKIRVISTILFILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGD 286
           :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     148 qkkqvsqtkirvistilfilagcivfvtipavifkyiegwtalesiyfvvvtlttvgfgd 207

Qy     287 FVAG----------------------------GNAGINYREWYKPLVWFWIL------ 310
           |||                            |  |||:| | |
Db     208 fvaahpsdhlcwvivtckgkyllpdspqekatdfsgvaqkrnepqkpliwcwelrsypta 267

Qy     311 --------------------------------VGLAYFA-AVLSMIGDWLRVLSKKTK 335
                                           |  |    ||||||||||||||||||
Db     268 lmmqervvxkekpkaaapnrrglgteklefxrxevaaavephavlsmigdwlrvlskktk 327

Qy     336 EE----------------------VGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQR 373
           ||                     ||||||||||||||||||||||||||||||||||
Db     328 eevcrpplfkspspnlrllgvahhvgeikahaaewkanvtaefretrrrlsveihdklqr 387

Qy     374 AATIRSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGP 433
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Db     388 aatirsmerrrlgldqrahsldmlspekrsvfaaldtgrfkassqesinnrpnnlrlkgp 447

Qy     434 EQLNKHGQGASEDNIINKFGSTSRLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEE 493
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    448 eqlnkhgqgasedniinkfgstsrltkrknkdlkktlpedvqkiyktfrnysldeekkee 507

Qy    494 ETEKMCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN 543
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    508 etekmcnsdnsstamltdciqqhaelengmiptdtkdrepennslledrn 557


RESULT   3
AAE10342
ID   AAE10342 standard; Protein; 411 AA.
XX
AC   AAE10342;
XX
DT   10-DEC-2001  (first entry)
XX
DE   Murine TREK-1 potassium channel protein.
XX
KW   Murine; potassium channel protein; TREK-1; anaesthetic; analgesia;
KW   amnesia.
XX
OS   Mus musculus.
XX
PN   WO200047738-A2.
XX
PD   17-AUG-2000.
XX
PF   11-FEB-2000; 2000WO-IB00226.
XX
PR   12-FEB-1999;   99US-0119727.
PR   11-FEB-2000; 2000US-0503089.
XX
PA   (CNRS ) CNRS CENT NAT RECH SCI.
XX
PI   Lazdunski M,  Honore E,  Lesage F,  Romey G,  Patel AJ;
XX
DR   WPI; 2000-549146/50.
DR   N-PSDB; AAD17497.
XX
PT   Novel nucleic acid encoding a TREK-1 potassium channel protein for
PT   transfecting cells to be used to identify compounds with anesthetic
PT   properties -
XX
PS   Claim 9; Page 32-33; 39pp; English.
XX
CC   The invention relates to human and mouse TREK-1 potassium channel
CC   proteins and their corresponding DNA molecules. TREK-1 nucleic acid is
CC   useful for transfecting cells to induce expression of the TREK-1
CC   potassium channel protein. These cells are then used in assays to
CC   identify compounds which have anaesthetic properties, producing a safe,
CC   reversible state of unconsciousness with concurrent amnesia and analgesia
CC   in a mammal upon inhalation. The present sequence is murine TREK-1
CC   potassium channel protein.
XX
SQ   Sequence   411 AA;


  Query Match           44.8%;  Score 1251.5;  DB 21;  Length 411;
  Best Local Similarity   64.3%;  Pred. No. 5.4e-105;
  Matches  247;  Conservative   54;  Mismatches   66;  Indels   17;  Gaps    5;

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Db      2 aapdlldpksa--------aqnskprlsfsskptvlasrvesds---ainvmkwktvsti 50

Qy     81 FVVVVVYLVTGGLVFRALEQPPESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD 140
          |:|||:||: |  ||:|||| | ||: || ::|  |:  | ||:  ||: |||  : |
Db     51 flvvvlyliigaavfkaleqpqeisqrttiviqkqtfiaqhacvnsteldeliqqivaai 110

Qy    141 NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF 200
          |||: |:|||||  |||||||:|||||||||||||:|||:| |||||||||:||: |||||
Db    111 nagiiplgnssnqvshwdlgssfffagtvittigfgnisprteggkifciiyallgiplf 170

Qy    201 GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF 260
          ||||||:|||||||||| ||:||  | |  |||||||:||||:||| ||::|| :|||||
Db    171 gfllagvgdqlgtifgkgiakvedtfikwnvsqtkiriistiifilfgcvlfvalpavif 230

Qy    261 KYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL 320
          |:||||:||::|||||:||||:||||:|||| : | | ::|||:|||||||||||||||
Db    231 khiegwsaldaiyfvvitlttigfgdyvagg-sdieyldfykpvvwfwilvglayfaavl 289

Qy    321 SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM 380
          |||||||||:|||||||||| :|||||| |||||||:|||||||||:|| ||| ::
Db    290 smigdwlrviskktkeevgefrahaaewtanvtaefketrrrlsveiydkfqratsv--- 346

Qy    381 ERRRLGLDQRAHSLDMLSPEKRSV 404
           :|:|  :   :    |:| :|::
Db    347 -krklsaelagnhnqeltpcrrti 369


RESULT   4
AAY28497
ID   AAY28497 standard; Protein; 411 AA.
XX
AC   AAY28497;
XX
DT   12-OCT-1999  (first entry)
XX
DE   Mouse h-TREK1 polypeptide.
XX
KW   h-TREK1; two pore potassium channel; inflammatory disease;
KW   chromosome 1q32.
XX
OS   Mus musculus.
XX
PN   WO9937762-A1.
XX
PD   29-JUL-1999.
XX
PF   02-DEC-1998;   98WO-EP07805.
XX
PR   09-OCT-1998;   98GB-0022135.
PR   27-JAN-1998;   98EP-0300570.
XX
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Chapman CG,  Meadows HJ;
XX
DR   WPI; 1999-469126/39.
DR   N-PSDB; AAZ00040.
XX
PT   New two pore potassium channel used for, e.g.  treatment of cancer,
PT   pulmonary, cardiovascular and inflammatory diseases
XX
PS   Claim 3; Page 26; 44pp; English.
XX
CC   This sequence is the mouse h-TREK1 polypeptide, encoded by the h-TREK1
CC   polynucleotide AAZ00040. h-TREK1 is a two pore potassium channel.
CC   The polynucleotide sequence of h-TREK1 can be used to diagnose a
CC   disease or susceptibility to a disease related to expression or activity
CC   of h-TREK-1 polypeptides. The methods of diagnosis may be used in the
CC   treatment of diseases including cancer, pulmonary, cardiovascular, and
CC   inflammatory diseases, pain, psychiatric disorders including depression
CC   and schizophrenia, neurodegenerative diseases including Alzheimer's,
CC   stroke, and head trauma and neurological disorders including migraine.
XX
SQ   Sequence   411 AA;


  Query Match           44.7%;  Score 1248.5;  DB 20;  Length 411;
  Best Local Similarity   64.3%;  Pred. No. 1e-104;
  Matches  247;  Conservative   53;  Mismatches   67;  Indels   17;  Gaps    5;

Qy     22 AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI 80
          ||  :  ||||        |    |||| ||: ||:| |:|  |      |||||||  |
Db      2 aapdlldpksa--------aqnskprlsfsskptvlasrvesds---ainvmkwktvsti 50
```

```
Qy      81 FVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD 140
           |:|||:||: |  ||:||||| | ||: || ::|  |:  | ||:  ||: |||  : |
Db      51 flvvvlyliigaavfkaleqpqeisqrttiviqkqtfiaqhacvnsteldeliqqivaai 110

Qy     141 NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF 200
           |||: |:|||||  |||||||:|||||||||||||:|||:| ||||||||||:||: |||||
Db     111 nagiiplgnssnqvshwdlgssfffagtvittigfgnisprteggkifciiyallgiplf 170

Qy     201 GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF 260
           ||||||:|||||||||| ||:||  | |  ||||||||:||||:||| ||::|| :|||||
Db     171 gfllagvgdqlgtifgkgiakvedtfikwnvsqtkiriistiifilfgcvlfvalpavif 230

Qy     261 KYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL 320
           |:||||:||::|||||:||||:||||:|||| : | | ::|||:|||||||||||||||||
Db     231 khiegwsaldaiyfvvitlttigfgdyvagg-sdieyldfykpvvwfwilvglayfaavl 289

Qy     321 SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM 380
           |||||||||:||||||,|||| :|||||| |||||||:|||||||||:|| ||| ::
Db     290 smigdwlrviskktkeevgefrahaaewtanvtaefketrrrlsveiydkfqratsv--- 346

Qy     381 ERRRLGLDQRAHSLDMLSPEKRSV 404
            :|:|  :   :    |:|  |::
Db     347 -krklsaelagnhnqeltpcmrtl 369
```

RESULT 5
AAY30648
ID AAY30648 standard; Protein; 370 AA.
XX
AC AAY30648;
XX
DT 18-NOV-1999 (first entry)
XX
DE A mechanically sensitive potassium channel protein TREK-1.
XX
KW Mechanically sensitive potassium channel protein; TREK-1;
KW polyunsaturated fatty acid; arachidonic acid; riluzole; heart disease;
KW nervous system disease; epilepsy; cardiovascular disease; arrhythmia;
KW neurodegeneration; ischemia; anoxia; hormone secretion abnormality;
KW muscular disease.
XX
OS Mus sp.
XX
PN WO9945108-A2.
XX
PD 10-SEP-1999.
XX
PF 23-FEB-1999; 99WO-FR00404.
XX
PR 05-MAR-1998; 98FR-0002725.
XX
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Honore E, Fink M, Lazdunski M, Lesage F, Duprat F;
XX
DR WPI; 1999-551038/46.
DR N-PSDB; AAZ10607.
XX
PT New mechanically sensitive potassium channel, used to screen for
PT specific modulators, potential therapeutic agents for heart and nervous
PT system disorders -
XX
PS Claim 3; Page 23-25; 40pp; French.
XX
CC The present sequence represents a mechanically sensitive potassium
CC channel protein designated TREK-1. The protein is activated by
CC polyunsaturated fatty acids, particularly arachidonic acid, and by
CC riluzole. The protein is used to screen for specific modulators which
CC are useful for treating or preventing diseases of the heart and nervous
CC systems in humans and animals, e.g. epilepsy, cardiovascular disease
CC (arrhythmia), neurodegeneration (particularly where associated with
CC ischemia or anoxia), abnormalities of hormone secretion and muscular
CC disease. The protein itself may be used to treat these diseases.
CC Antibodies specific for the protein are used to detect it in tissues,
CC also as therapeutic inhibitors or activators.
XX
SQ Sequence 370 AA;

```
  Query Match             44.6%;  Score 1247.5;  DB 20;  Length 370;
  Best Local Similarity   64.5%;  Pred. No. 1.1e-104;
  Matches  247;  Conservative   52;  Mismatches   67;  Indels   17;  Gaps    5;

Qy      22 AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI 80
           ||  :  ||||        |    |||| ||: ||:| |:|  |     |||||||  |
Db       2 aapdlldpksa--------aqnskprlsfsskptvlasrvesds---ainvmkwktvsti 50

Qy      81 FVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD 140
           |:|||:||: |  ||:||||| | ||: || ::|  |:  | ||:  ||: |||  : |
Db      51 flvvvlyliigaavfkaleqpqeisqrttiviqkqtfiaqhacvnsteldeliqqivaai 110

Qy     141 NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF 200
           |||: |:|||||  |||||||:|||||||||||||:|||:| ||||||||||:||: |||||
Db     111 nagiiplgnssnqvshwdlgssfffagtvittigfgnisprteggkifciiyallgiplf 170

Qy     201 GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF 260
           ||||||:|||||||||| ||:||  | |  ||||||||:||||:||| ||::|| :|||||
Db     171 gfllagvgdqlgtifgkgiakvedtfikwnvsqtkiriistiifilfgcvlfvalpavif 230

Qy     261 KYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL 320
           |:||||:||::|||||:||||:||||:|||| : | | ::|||:|||||||||||||||||
Db     231 khiegwsaldaiyfvvitlttigfgdyvagg-sdieyldfykpvvwfwilvglayfaavl 289

Qy     321 SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM 380
           |||||||||:||||||||| :|||||| |||||||:|||||||||:|| ||| ::
Db     290 smigdwlrviskktkeevgefrahaaewtanvtaefketrrrlsveiydkfqratsv--- 346

Qy     381 ERRRLGLDQRAHSLDMLSPEKRS 403
            :|:|  :   :    |:|  |:
Db     347 -krklsaelagnhnqeltpcmrt 368
```

RESULT 6
AAE10341
ID AAE10341 standard; Protein; 411 AA.
XX
AC AAE10341;
XX
DT 10-DEC-2001 (first entry)
XX
DE Human TREK-1 potassium channel protein.
XX
KW Human; potassium channel protein; TREK-1; anaesthetic; analgesia;
KW amnesia.
XX
OS Homo sapiens.
XX
PN WO200047738-A2.
XX
PD 17-AUG-2000.
XX
PF 11-FEB-2000; 2000WO-IB00226.
XX
PR 12-FEB-1999; 99US-0119727.
PR 11-FEB-2000; 2000US-0503089.
XX
PA (CNRS) CNRS CENT NAT RECH SCI.
XX
PI Lazdunski M, Honore E, Lesage F, Romey G, Patel AJ;
XX
DR WPI; 2000-549146/50.
DR N-PSDB; AAD17496.
XX
PT Novel nucleic acid encoding a TREK-1 potassium channel protein for
PT transfecting cells to be used to identify compounds with anesthetic

```
PT   properties -
XX
PS   Claim 3; Page 28; 39pp; English.
XX
CC   The invention relates to human and mouse TREK-1 potassium channel
CC   proteins and their corresponding DNA molecules. TREK-1 nucleic acid is
CC   useful for transfecting cells to induce expression of the TREK-1
CC   potassium channel protein. These cells are then used in assays to
CC   identify compounds which have anaesthetic properties, producing a safe,
CC   reversible state of unconsciousness with concurrent amnesia and analgesia
CC   in a mammal upon inhalation. The present sequence is human TREK-1
CC   potassium channel protein.
XX
SQ   Sequence   411 AA;


  Query Match             44.5%;  Score 1243;  DB 21;  Length 411;
  Best Local Similarity   62.7%;  Pred. No. 3.2e-104;
  Matches  247;  Conservative   54;  Mismatches   65;  Indels   28;  Gaps    6;

Qy      22 AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI 80
           ||  :  ||||        |    |||| |:: ||:| |:|  :      |||||||  |
Db       2 aapdlldpksa--------aqnskprlsfstkptvlasrvesdt---tinvmkwktvsti 50

Qy      81 FVVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD 140
           |:|||:||: |  ||:|||| | ||: || ::|  |:  | ||:  ||: |||  : |
Db      51 flvvvlyliigatvfkaleqpheisqrttiviqkqtfisqhscvnsteldeliqqivaai 110

Qy     141 NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF 200
           |||: |:||:||  |||||||:||||||||||||:|||:| |||||||||:||: |||||
Db     111 nagiiplgntsnqishwdlgssfffagtvittigfgnisprteggkifciiyallgiplf 170

Qy     201 GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF 260
           ||||||:|||||||||| ||:||  | |  |||||||:||||:||| ||::|| :||:||
Db     171 gfllagvgdqlgtifgkgiakvedtfikwnvsqtkiriistiifilfgcvlfvalpaiif 230

Qy     261 KYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL 320
           |:||||:||::|||||:||||:||||:|||| : | | ::|||:|||||||||||||||
Db     231 khiegwsaldaiyfvvitlttigfgdyvagg-sdieyldfykpvvwfwilvglayfaavl 289

Qy     321 SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIR-- 378
           |||||||||:|||||||||| :|||||| |||||||:|||||||||:|| ||| :|:
Db     290 smigdwlrviskktkeevgefrahaaewtanvtaefketrrrlsveiydkfqratsikrk 349

Qy     379 -SME------------RRRLGLDQRAHSLDMLSP 399
            | |            || | ::   :  |:| |
Db     350 lsaelagnhnqeltpcrrtlsvnhltnerdvlpp 383


RESULT   7
AAY34133
ID   AAY34133 standard; Protein; 411 AA.
XX
AC   AAY34133;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human potassium channel K+Hnov59.
XX
KW   Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;
KW   cardiovascular disorder; CNS disorder; renal disorder.
XX
OS   Homo sapiens.
XX
PN   WO9943696-A1.
XX
PD   02-SEP-1999.
XX
PF   22-FEB-1999;   99WO-US03826.
XX
PR   19-JAN-1999;   99US-0116448.
PR   25-FEB-1998;   98US-0076687.
PR   07-AUG-1998;   98US-0095836.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Curran ME,  Hu P,  Miller AP,  Rutter M,  Wang J;
XX
DR   WPI; 1999-527591/44.
DR   N-PSDB; AAZ11915.
XX
PT   New nucleic acids encoding mammalian K+Hnov potassium channel
PT   proteins, useful for the diagnosis and treatment of episodic ataxia
PT   with myokymia, cardiac arrhythmia, epilepsy and Bartter's syndrome
XX
PS   Claim 3; Page 104-105; 112pp; English.
XX
CC   This sequence represents the human K+Hnov59 potassium channel.
CC   K+Hnov proteins have a high degree of homology to known potassium
CC   channels and may be alpha subunits, which form the functional channel,
CC   or accessory subunits that act to modulate the channel activity. K+Hnov59
CC   is a 4 transmembrane domain, 2 pore domain potassium channel. The gene
CC   is located on chromosome 19, determined via PCR chromosomal
CC   localisation using primers AAZ11939 and AAZ11940. K+Hnov cDNAs
CC   were isolated by extension of expressed sequence tags (ESTs) which were
CC   related but not identical to known human potassium channels. Potential
CC   polymorphisms detected as sequence variants between multiple
CC   independent clones. Potassium channels have critical roles in various
CC   cell types and biochemical pathways. Defective potassium channels are
CC   known to cause four human diseases: episodic ataxia with myokymia;
CC   cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's syndrome.
CC   As potassium channels are critical components of virtually all cells,
CC   it is likely that abnormal potassium channels are also implicated in
CC   certain renal, cardiovascular and central nervous system (CNS)
CC   disorders. Nucleotides encoding K+Hnov proteins may be used for
CC   identifying homologous or related proteins and the DNA sequences encoding
CC   them. They may be used to produce compositions that modulate the
CC   expression and function of the K+Hnov protein and in studying the
CC   biochemical pathways associated with it. They may also be used for the
CC   recombinant production of K+Hnov protein in fermentation cultures.
CC   Additionally, such nucleotides may be used in gene therapy protocols for
CC   the treatment of diseases associated with abnormal potassium channels.
XX
SQ   Sequence   411 AA;


  Query Match             44.5%;  Score 1242.5;  DB 20;  Length 411;
  Best Local Similarity   63.5%;  Pred. No. 3.5e-104;
  Matches  244;  Conservative   57;  Mismatches   66;  Indels   17;  Gaps    5;

Qy      22 AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI 80
           ||  :  ||||        |    |||| |:: ||:| |:|  :      |||||||  |
Db       2 aapdlldpksa--------aqnskprlsfstkptvlasrvesdt---tinvmkwktvsti 50

Qy      81 FVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD 140
           |:|||:||: |  ||:|||| | ||: || ::|  |:  | ||:  ||: |||  : |
Db      51 flvvvlyliigatvfkaleqpheisqrttiviqkqtfisqhscvnsteldeliqqivaai 110

Qy     141 NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF 200
           |||: |:||:||  |||||||:||||||||||||:|||:| |||||||||:||: |||||
Db     111 nagiiplgntsnqishwdlgssfffagtvittigfgnisprteggkifciiyallgiplf 170

Qy     201 GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF 260
           ||||||:|||||||||| ||:||  | |  |||||||:||||:||| ||::|| :||:||
Db     171 gfllagvgdqlgtifgkgiakvedtfikwnvsqtkiriistiifilfgcvlfvalpaiif 230

Qy     261 KYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL 320
           |:||||:||::|||||:||||:||||:|||| : | | ::|||:|||||||||||||||
Db     231 khiegwsaldaiyfvvitlttigfgdyvagg-sdieyldfykpvvwfwilvglayfaavl 289

Qy     321 SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM 380
           |||||||||:|||||||||| :|||||| |||||||:|||||||||:|| ||| :|
Db     290 smigdwlrviskktkeevgefrahaaewtanvtaefketrrrlsveiydkfqratsi--- 346

Qy     381 ERRRLGLDQRAHSLDMLSPEKRSV 404
            :|:|  :   :    |:| :|::
```

```
Db    347 -krklsaelagnhnqeltpcrrtl 369


RESULT   8
AAY28496
ID   AAY28496 standard; Protein; 411 AA.
XX
AC   AAY28496;
XX
DT   12-OCT-1999  (first entry)
XX
DE   h-TREK1 polypeptide.
XX
KW   h-TREK1; two pore potassium channel; inflammatory disease;
KW   chromosome 1q32.
XX
OS   Homo sapiens.
XX
PN   WO9937762-A1.
XX
PD   29-JUL-1999.
XX
PF   02-DEC-1998;   98WO-EP07805.
XX
PR   09-OCT-1998;   98GB-0022135.
PR   27-JAN-1998;   98EP-0300570.
XX
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Chapman CG,  Meadows HJ;
XX
DR   WPI; 1999-469126/39.
DR   N-PSDB; AAZ00039.
XX
PT   New two pore potassium channel used for, e.g.  treatment of cancer,
PT   pulmonary, cardiovascular and inflammatory diseases
XX
PS   Claim 3; Page 24; 44pp; English.
XX
CC   This sequence is the h-TREK1 polypeptide, encoded by the h-TREK1
CC   polynucleotide AAZ00039. h-TREK1 is a two pore potassium channel, and
CC   the gene maps to human chromosome 1q32, between the markers D1S237 and
CC   WI5105. The polynucleotide sequence of h-TREK1 can be used to diagnose a
CC   disease or susceptibility to a disease related to expression or activity
CC   of h-TREK-1 polypeptides. The methods of diagnosis may be used in the
CC   treatment of diseases including cancer, pulmonary, cardiovascular, and
CC   inflammatory diseases, pain, psychiatric disorders including depression
CC   and schizophrenia, neurodegenerative diseases including Alzheimer's,
CC   stroke, and head trauma and neurological disorders including migraine.
XX
SQ   Sequence   411 AA;


  Query Match             44.5%;  Score 1242.5;  DB 20;  Length 411;
  Best Local Similarity   63.5%;  Pred. No. 3.5e-104;
  Matches  244;  Conservative   57;  Mismatches   66;  Indels   17;  Gaps    5;

Qy      22 AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI 80
           ||  :  ||||       |    |||| |:: ||:| |:|  :     |||||||  |
Db       2 aapdlldpksa--------aqnskprlsfstkptvlasrvesdt---tinvmkwktvsti 50

Qy      81 FVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD 140
           |:|||:||: |  ||:|||| | ||: || ::|  |:  | ||:  ||: |||  : |
Db      51 flvvvlyliigatvfkaleqpheisqrttiviqkqtfisqhscvnsteldeliqqivaai 110

Qy     141 NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF 200
           |||: |:||:|| |||||||:|||||||||||||:|||:| |||||||||:||: |||||
Db     111 nagiiplgntsnqishwdlgssfffagtvittigfgnisprteggkifciiyallgiplf 170

Qy     201 GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF 260
           ||||||:|||||||||| ||:||  | |  |||||||:||||:||| ||::|| :||:||
Db     171 gfllagvgdqlgtifgkgiakvedtfikwnvsqtkiriistiifilfgcvlfvalpaiif 230

Qy     261 KYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL 320
           |:||||:||::|||||:||||:||||:|||| : | | ::|||:|||||||||||||||
Db     231 khiegwsaldaiyfvvitlttigfgdyvagg-sdieyldfykpvvwfwilvglayfaavl 289

Qy     321 SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM 380
           |||||||||:|||||||||| :|||||| |||||||:||||||||||:|| ||| :|
Db     290 smigdwlrviskktkeevgefrahaaewtanvtaefketrrrlsveiydkfqratsi--- 346

Qy     381 ERRRLGLDQRAHSLDMLSPEKRSV 404
           :|:|  :   :    |:| :|::
Db     347 -krklsaelagnhnqeltpcrrtl 369


RESULT   9
AAB50044
ID   AAB50044 standard; Protein; 411 AA.
XX
AC   AAB50044;
XX
DT   19-MAR-2001  (first entry)
XX
DE   Human TREK.
XX
KW   Human; TREK; 2P domain potassium channel; resting membrane potential;
KW   neuronal excitability; neurotransmitter release modulation; epilepsy;
KW   neurological disorder; sleep-related disorder; cognitive dysfunction;
KW   attention deficit disorder; addiction; anxiety; phobia;
KW   Parkinson's chorea; Huntington's chorea; cerebral palsy; incontinence;
KW   erectile dysfunction; alopecia.
XX
OS   Homo sapiens.
XX
PN   WO200072863-A2.
XX
PD   07-DEC-2000.
XX
PF   01-JUN-2000; 2000WO-GB02107.
XX
PR   01-JUN-1999;   99GB-0012733.
XX
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI   Hervieu GJ,  Meadows HJ,  Randall AD;
XX
DR   WPI; 2001-080422/09.
DR   N-PSDB; AAC90412.
XX
PT   Use of human TREK1 polypeptide, polynucleotides encoding them and
PT   modulators of h-TREK1 polypeptides for treating epilepsy, sleep-related
PT   disorders, addiction and dyskinesias including Parkinson's and
PT   Huntington's chorea  -
XX
PS   Claim 7; Page 29; 35pp; English.
XX
CC   The present sequence is human TREK1 (h-TREK1). h-TREK1 is a member of the
CC   2P domain potassium channel family of proteins which play a part in the
CC   control of resting membrane potential. Modulation of these channels will
CC   therefore affect neuronal excitability, thereby leading to a modulation
CC   of neurotransmitter release and activity of neuronal networks. Such
CC   modulation therefore may be useful for the treatment of certain
CC   neurological conditions such as epilepsy, sleep-related disorders,
CC   cognitive dysfunction, attention deficit disorder, addiction,
CC   anxiety/phobia, Parkinson's and Huntington's chorea, cerebral palsy,
CC   incontinence, erectile dysfunction or alopecia.
XX
SQ   Sequence   411 AA;


  Query Match             44.5%;  Score 1242.5;  DB 22;  Length 411;
  Best Local Similarity   63.5%;  Pred. No. 3.5e-104;
  Matches  244;  Conservative   57;  Mismatches   66;  Indels   17;  Gaps    5;

Qy      22 AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI 80
```

```
          ||  :  ||||        |    |||| |:: ||:| |:|  :      |||||||  |
Db      2 aapdlldpksa--------aqnskprlsfstkptvlasrvesdt---tinvmkwktvsti 50

Qy     81 FVVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD 140
          |:|||:||: |  ||:|||||  | ||: || ::|  |:  | ||:  ||: |||  : |
Db     51 flvvvlyliigatvfkaleqpheisqrttiviqkqtfisqhscvnsteldeliqqivaai 110

Qy    141 NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF 200
          |||: |:||:||  |||||||:||||||||||||:|||:| |||||||||:||: |||||
Db    111 nagiiplgntsnqishwdlgssfffagtvittigfgnisprteggkifciiyallgiplf 170

Qy    201 GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF 260
          ||||||:|||||||||| ||:||  | |  |||||||:||||:||| ||::|| :||:||
Db    171 gfllagvgdqlgtifgkgiakvedtfikwnvsqtkiriistiifilfgcvlfvalpaiif 230

Qy    261 KYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL 320
          |:||||:||::|||||:||||:||||:|||| : | | ::|||:|||||||||||||||
Db    231 khiegwsaldaiyfvvitlttigfgdyvagg-sdieyldfykpvvwfwilvglayfaavl 289

Qy    321 SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM 380
          |||||||||:|||||||||| :|||||| |||||||:||||||||||:|| ||| :|
Db    290 smigdwlrviskktkeevgefrahaaewtanvtaefketrrrlsveiydkfqratsi--- 346

Qy    381 ERRRLGLDQRAHSLDMLSPEKRSV 404
           :|:|  :   :    |:| :|::
Db    347 -krklsaelagnhnqeltpcrrtl 369
```

RESULT 10
AAU07618
ID AAU07618 standard; Protein; 426 AA.
XX
AC AAU07618;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human potassium ion channel TPKC1 protein.
XX
KW Transmembrane potassium ion channel protein; inward potassium flux;
KW pest control; membrane potential; pesticide; antihelminthic; nematode;
KW insect; TPKC1; human.
XX
OS Homo sapiens.
XX
PN WO200161006-A2.
XX
PD 23-AUG-2001.
XX
PF 14-FEB-2001; 2001WO-US04680.
XX
PR 15-FEB-2000; 2000US-0503849.
XX
PA (BADI) BASF CORP.
XX
PI Pausch MH;
XX
DR WPI; 2001-536570/59.
DR N-PSDB; AAS12169.
XX
PT New polypeptide, a mutant potassium ion channel protein for improving
PT inward potassium flux under acidic conditions -
XX
PS Example 15; Page 45; 131pp; English.
XX
CC The invention relates to a mutant potassium ion channel protein, having
CC four membrane spanning domains and two pore forming domains, comprising a
CC mutation at the second pore forming domain. The expression of the mutant
CC protein in a cell confers improved inward potassium flux and the ability
CC to grow in the presence of potassium. Mutant proteins and their
CC corresponding polynucleotide sequences can therefore be used to improve
CC inward potassium flux into cells under acidic conditions by modulating
CC the membrane potential using therapeutic agents. The sequences may be
CC used to develop agonists and antagonists of potassium channel proteins in
CC order to control pests such as nematodes and insects. This sequence
CC represents a human transmembrane potassium ion channel protein, TPKC1.
XX
SQ Sequence 426 AA;

Query Match 43.6%; Score 1218.5; DB 22; Length 426;
Best Local Similarity 62.8%; Pred. No. 5.6e-102;
Matches 241; Conservative 58; Mismatches 68; Indels 17; Gaps 5;

```
Qy     22 AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI 80
          ||  :  ||||        |    |||| |:: ||:| |:|  :      |||||||  |
Db     17 aapdlldpksa--------aqnskprlsfstkptvlasrvesdt---tinvmkwktvsti 65

Qy     81 FVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD 140
          |:|||:||: |  ||:|||||  | ||: || ::|  |:  | ||:  ||: |||  : |
Db     66 flvvvlyliigatvfkaleqpheisqrttiviqkqtfisqhscvnsteldeliqqivaai 125

Qy    141 NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF 200
          |||: |:||:||  |||||||:||||||||||||:|||:| |||||||||:||: |||||
Db    126 nagiiplgntsnqishwdlgssfffagtvittigfgnisprteggkifciiyallgiplf 185

Qy    201 GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF 260
          ||||||:|||||||||| ||:||  | |  |||||||:||||:||| ||::|| :||:||
Db    186 gfllagvgdqlgtifgkgiakvedtfikwnvsqtkiriistiifilfgcvlfvalpaiif 245

Qy    261 KYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL 320
          |:||||:||::|||||:||||:||||:|||| : | | ::|||:|||||||||||||||
Db    246 khiegwsaldaiyfvvitlttigfgdyvagg-sdieyldfykpvvwfwilvglayfaavl 304

Qy    321 SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM 380
          ||||  :||:|||||||||| :|||||| |||||||:||||||||||:|| ||| :|
Db    305 smigrlvrviskktkeevgefrahaaewtanvtaefketrrrlsveiydkfqratsi--- 361

Qy    381 ERRRLGLDQRAHSLDMLSPEKRSV 404
           :|:|  :   :    |:| :|::
Db    362 -krklsaelagnhnqeltpcrrtl 384
```

RESULT 11
AAU07622
ID AAU07622 standard; Protein; 426 AA.
XX
AC AAU07622;
XX
DT 21-NOV-2001 (first entry)
XX
DE Human potassium ion channel TPKC1 mutant protein #1.
XX
KW Transmembrane potassium ion channel protein; inward potassium flux;
KW pest control; membrane potential; pesticide; antihelminthic; nematode;
KW insect; TPKC1; human; mutant; mutein.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 256
FT /note= "Wild-type Ala replaced by Thr"
XX
PN WO200161006-A2.
XX
PD 23-AUG-2001.
XX
PF 14-FEB-2001; 2001WO-US04680.
XX
PR 15-FEB-2000; 2000US-0503849.
XX
PA (BADI) BASF CORP.
XX
PI Pausch MH;
XX
DR WPI; 2001-536570/59.
DR N-PSDB; AAS12181.

```
XX
PT   New polypeptide, a mutant potassium ion channel protein for improving
PT   inward potassium flux under acidic conditions  -
XX
PS   Claim 37; Page 113-115; 131pp; English.
XX
CC   The invention relates to a mutant potassium ion channel protein, having
CC   four membrane spanning domains and two pore forming domains, comprising a
CC   mutation at the second pore forming domain. The expression of the mutant
CC   protein in a cell confers improved inward potassium flux and the ability
CC   to grow in the presence of potassium. Mutant proteins and their
CC   corresponding polynucleotide sequences can therefore be used to improve
CC   inward potassium flux into cells under acidic conditions by modulating
CC   the membrane potential using therapeutic agents. The sequences may be
CC   used to develop agonists and antagonists of potassium channel proteins in
CC   order to control pests such as nematodes and insects. This sequence
CC   represents a human transmembrane potassium ion channel TPKC1 mutant
CC   protein.
XX
SQ   Sequence   426 AA;


  Query Match             43.6%;  Score 1218.5;  DB 22;  Length 426;
  Best Local Similarity   62.8%;  Pred. No. 5.6e-102;
  Matches  241;  Conservative   58;  Mismatches   68;  Indels   17;  Gaps    5;

Qy      22 AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI 80
           ||  :  ||||         |    |||| |:: ||:| |:|  :       |||||||  |
Db      17 aapdlldpksa--------aqnskprlsfstkptvlasrvesdt---tinvmkwktvsti 65

Qy      81 FVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD 140
           |:|||:||: |  ||:||||| | ||: || ::|  |:  | ||:  ||: |||  : |
Db      66 flvvvlyliigatvfkaleqpheisqrttiviqkqtfisqhscvnsteldeliqqivaai 125

Qy     141 NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF 200
           |||: |:||:||  |||||||:||||||||||||:|||:| |||||||||:||: |||||
Db     126 nagiiplgntsnqishwdlgssfffagtvittigfgnisprteggkifciiyallgiplf 185

Qy     201 GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF 260
           ||||||:|||||||||| ||:||  | |  |||||||:||||:||| ||::|| :||:||
Db     186 gfllagvgdqlgtifgkgiakvedtfikwnvsqtkiriistiifilfgcvlfvalpaiif 245

Qy     261 KYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL 320
           |:||||:||::|||||:||||:||||:|||| : | | ::|||:||||||||||||||||
Db     246 khiegwsaldtiyfvvitlttigfgdyvagg-sdieyldfykpvvwfwilvglayfaavl 304

Qy     321 SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM 380
           ||||  :||:|||||||||| :|||||| |||||||:|||||||||||:|| ||| :|
Db     305 smigrlvrviskktkeevgefrahaaewtanvtaefketrrrlsveiydkfqratsi--- 361

Qy     381 ERRRLGLDQRAHSLDMLSPEKRSV 404
            :|:|  :   :    |:| :|::
Db     362 -krklsaelagnhnqeltpcrrtl 384


RESULT  12
AAU07623
ID   AAU07623 standard; Protein; 426 AA.
XX
AC   AAU07623;
XX
DT   21-NOV-2001  (first entry)
XX
DE   Human potassium ion channel TPKC1 mutant protein #2.
XX
KW   Transmembrane potassium ion channel protein; inward potassium flux;
KW   pest control; membrane potential; pesticide; antihelminthic; nematode;
KW   insect; TPKC1; human; mutant; mutein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 272
FT                   /note= "Wild-type Tyr replaced by His"
XX
PN   WO200161006-A2.
XX
PD   23-AUG-2001.
XX
PF   14-FEB-2001; 2001WO-US04680.
XX
PR   15-FEB-2000; 2000US-0503849.
XX
PA   (BADI ) BASF CORP.
XX
PI   Pausch MH;
XX
DR   WPI; 2001-536570/59.
DR   N-PSDB; AAS12182.
XX
PT   New polypeptide, a mutant potassium ion channel protein for improving
PT   inward potassium flux under acidic conditions  -
XX
PS   Claim 37; Page 115-117; 131pp; English.
XX
CC   The invention relates to a mutant potassium ion channel protein, having
CC   four membrane spanning domains and two pore forming domains, comprising a
CC   mutation at the second pore forming domain. The expression of the mutant
CC   protein in a cell confers improved inward potassium flux and the ability
CC   to grow in the presence of potassium. Mutant proteins and their
CC   corresponding polynucleotide sequences can therefore be used to improve
CC   inward potassium flux into cells under acidic conditions by modulating
CC   the membrane potential using therapeutic agents. The sequences may be
CC   used to develop agonists and antagonists of potassium channel proteins in
CC   order to control pests such as nematodes and insects. This sequence
CC   represents a human transmembrane potassium ion channel TPKC1 mutant
CC   protein.
XX
SQ   Sequence   426 AA;


  Query Match             43.5%;  Score 1214.5;  DB 22;  Length 426;
  Best Local Similarity   62.8%;  Pred. No. 1.3e-101;
  Matches  241;  Conservative   57;  Mismatches   69;  Indels   17;  Gaps    5;

Qy      22 AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI 80
           ||  :  ||||         |    |||| |:: ||:| |:|  :       |||||||  |
Db      17 aapdlldpksa--------aqnskprlsfstkptvlasrvesdt---tinvmkwktvsti 65

Qy      81 FVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD 140
           |:|||:||: |  ||:||||| | ||: || ::|  |:  | ||:  ||: |||  : |
Db      66 flvvvlyliigatvfkaleqpheisqrttiviqkqtfisqhscvnsteldeliqqivaai 125

Qy     141 NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF 200
           |||: |:||:||  |||||||:||||||||||||:|||:| |||||||||:||: |||||
Db     126 nagiiplgntsnqishwdlgssfffagtvittigfgnisprteggkifciiyallgiplf 185

Qy     201 GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF 260
           ||||||:|||||||||| ||:||  | |  |||||||:||||:||| ||::|| :||:||
Db     186 gfllagvgdqlgtifgkgiakvedtfikwnvsqtkiriistiifilfgcvlfvalpaiif 245

Qy     261 KYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL 320
           |:||||:||::|||||:||||:||||:|||| : | | ::|||:||||||||||||||||
Db     246 khiegwsaldaiyfvvitlttigfgdhvagg-sdieyldfykpvvwfwilvglayfaavl 304

Qy     321 SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM 380
           ||||  :||:|||||||||| :|||||| |||||||:|||||||||||:|| ||| :|
Db     305 smigrlvrviskktkeevgefrahaaewtanvtaefketrrrlsveiydkfqratsi--- 361

Qy     381 ERRRLGLDQRAHSLDMLSPEKRSV 404
            :|:|  :   :    |:| :|::
Db     362 -krklsaelagnhnqeltpcrrtl 384


RESULT  13
AAU07624
```

```
ID   AAU07624 standard; Protein; 426 AA.
XX
AC   AAU07624;
XX
DT   21-NOV-2001  (first entry)
XX
DE   Human potassium ion channel TPKC1 mutant protein #3.
XX
KW   Transmembrane potassium ion channel protein; inward potassium flux;
KW   pest control; membrane potential; pesticide; antihelminthic; nematode;
KW   insect; TPKC1; human; mutant; mutein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 272
FT                   /note= "Wild-type Tyr replaced by His"
FT   Misc-difference 274
FT                   /note= "Wild-type Ala replace by Val"
XX
PN   WO200161006-A2.
XX
PD   23-AUG-2001.
XX
PF   14-FEB-2001; 2001WO-US04680.
XX
PR   15-FEB-2000; 2000US-0503849.
XX
PA   (BADI ) BASF CORP.
XX
PI   Pausch MH;
XX
DR   WPI; 2001-536570/59.
DR   N-PSDB; AAS12183.
XX
PT   New polypeptide, a mutant potassium ion channel protein for improving
PT   inward potassium flux under acidic conditions  -
XX
PS   Claim 37; Page 117-119; 131pp; English.
XX
CC   The invention relates to a mutant potassium ion channel protein, having
CC   four membrane spanning domains and two pore forming domains, comprising a
CC   mutation at the second pore forming domain. The expression of the mutant
CC   protein in a cell confers improved inward potassium flux and the ability
CC   to grow in the presence of potassium. Mutant proteins and their
CC   corresponding polynucleotide sequences can therefore be used to improve
CC   inward potassium flux into cells under acidic conditions by modulating
CC   the membrane potential using therapeutic agents. The sequences may be
CC   used to develop agonists and antagonists of potassium channel proteins in
CC   order to control pests such as nematodes and insects. This sequence
CC   represents a human transmembrane potassium ion channel TPKC1 mutant
CC   protein.
XX
SQ   Sequence   426 AA;


  Query Match           43.3%;  Score 1210.5;  DB 22;  Length 426;
  Best Local Similarity   62.5%;  Pred. No. 3e-101;
  Matches  240;  Conservative   57;  Mismatches   70;  Indels   17;  Gaps    5;

Qy      22 AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI 80
           ||  :  ||||        |    |||| |:: ||:| |:|  :      |||||||  |
Db      17 aapdlldpksa--------aqnskprlsfstkptvlasrvesdt---tinvmkwktvsti 65

Qy      81 FVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD 140
           |:|||:||: |  ||:||||| | ||: || ::|  |:  | ||:  ||: |||  : |
Db      66 flvvvlyliigatvfkaleqpheisqrttiviqkqtfisqhscvnsteldeliqqivaai 125

Qy     141 NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF 200
           |||: |:||:||  |||||||:||||||||||||:|||:| |||||||||:||: |||||
Db     126 nagiiplgntsnqishwdlgssfffagtvittigfgnisprteggkifciiyallgiplf 185

Qy     201 GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF 260
           ||||||:|||||||||| ||:||  | |  |||||||:||||:||| ||::|| :||:||
Db     186 gfllagvgdqlgtifgkgiakvedtfikwnvsqtkiriistiifilfgcvlfvalpaiif 245

Qy     261 KYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL 320
           |:||||:||::|||||:||||:|||| | || : | | ::|||:|||||||||||||||
Db     246 khiegwsaldaiyfvvitlttigfgdhvvgg-sdieyldfykpvvwfwilvglayfaavl 304

Qy     321 SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM 380
           ||||  :||:|||||||||| :|||||| |||||||:||||||||||:|| ||| :|
Db     305 smigrlvrviskktkeevgefrahaaewtanvtaefketrrrlsveiydkfqratsi--- 361

Qy     381 ERRRLGLDQRAHSLDMLSPEKRSV 404
           :|:|  :   :    |:| :|::
Db     362 -krklsaelagnhnqeltpcrrtl 384


RESULT  14
AAU07625
ID   AAU07625 standard; Protein; 426 AA.
XX
AC   AAU07625;
XX
DT   21-NOV-2001  (first entry)
XX
DE   Human potassium ion channel TPKC1 mutant protein #4.
XX
KW   Transmembrane potassium ion channel protein; inward potassium flux;
KW   pest control; membrane potential; pesticide; antihelminthic; nematode;
KW   insect; TPKC1; human; mutant; mutein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 270
FT                   /note= "Wild-type Gly replaced by Arg"
XX
PN   WO200161006-A2.
XX
PD   23-AUG-2001.
XX
PF   14-FEB-2001; 2001WO-US04680.
XX
PR   15-FEB-2000; 2000US-0503849.
XX
PA   (BADI ) BASF CORP.
XX
PI   Pausch MH;
XX
DR   WPI; 2001-536570/59.
DR   N-PSDB; AAS12184.
XX
PT   New polypeptide, a mutant potassium ion channel protein for improving
PT   inward potassium flux under acidic conditions  -
XX
PS   Claim 37; Page 119-120; 131pp; English.
XX
CC   The invention relates to a mutant potassium ion channel protein, having
CC   four membrane spanning domains and two pore forming domains, comprising a
CC   mutation at the second pore forming domain. The expression of the mutant
CC   protein in a cell confers improved inward potassium flux and the ability
CC   to grow in the presence of potassium. Mutant proteins and their
CC   corresponding polynucleotide sequences can therefore be used to improve
CC   inward potassium flux into cells under acidic conditions by modulating
CC   the membrane potential using therapeutic agents. The sequences may be
CC   used to develop agonists and antagonists of potassium channel proteins in
CC   order to control pests such as nematodes and insects. This sequence
CC   represents a human transmembrane potassium ion channel TPKC1 mutant
CC   protein.
XX
SQ   Sequence   426 AA;


  Query Match           43.3%;  Score 1210.5;  DB 22;  Length 426;
```

```
  Best Local Similarity   62.5%;  Pred. No. 3e-101;
  Matches  240;  Conservative   58;  Mismatches   69;  Indels   17;  Gaps    5;

Qy      22 AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI 80
           ||  :  ||||        |    |||| ||:: ||:| |:|  :      |||||||  |
Db      17 aapdlldpksa--------aqnskprlsfstkptvlasrvesdt---tinvmkwktvsti 65

Qy      81 FVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD 140
           |:|||:||: |  ||:|||||| | ||: || ::|  |:  | ||:  ||: |||  : |
Db      66 flvvvlyliigatvfkaleqpheisqrttiviqkqtfisqhscvnsteldeliqqivaai 125

Qy     141 NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF 200
           |||: |:||:||  |||||||:||||||||||||:|||:| ||||||||:||: |||||
Db     126 nagiiplgntsnqishwdlgssfffagtvittigfgnisprteggkifciiyallgiplf 185

Qy     201 GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF 260
           ||||||:|||||||||| ||:||  | |  |||||||:||||:||| ||::|| :||:||
Db     186 gfllagvgdqlgtifgkgiakvedtfikwnvsqtkiriistiifilfgcvlfvalpaiif 245

Qy     261 KYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL 320
           |:||||:||::|||||:||||:|| |:|||| : | | ::|||:|||||||||||||||
Db     246 khiegwsaldaiyfvvitlttigfrdyvagg-sdieyldfykpvvwfwilvglayfaavl 304

Qy     321 SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM 380
           ||||  :||:|||||||||| :|||||| |||||||:||||||||||:|| ||| :|
Db     305 smigrlvrviskktkeevgefrahaaewtanvtaefketrrrlsveiydkfqratsi--- 361

Qy     381 ERRRLGLDQRAHSLDMLSPEKRSV 404
            :|:|  :   :    |:| :|::
Db     362 -krklsaelagnhnqeltpcrrtl 384


RESULT  15
AAU04571
ID   AAU04571 standard; Protein; 1314 AA.
XX
AC   AAU04571;
XX
DT   17-DEC-2001  (first entry)
XX
DE   Human G-protein coupled receptor like protein, GPCR #8.
XX
KW   Human; G-protein coupled receptor like protein; GPCR; immunogen;
KW   ophthalmic disease; neurological disease; Alzheimer's disease;
KW   Parkinson's disease; immunological disorder; HIV; candidiasis;
KW   human immunodeficiency virus; autoimmune disorder; multiple sclerosis;
KW   systemic lupus erythematosus; rheumatoid arthritis; platelet disorder;
KW   thrombocytopaenia; aplastic anaemia; inflammatory disorder;
KW   septic shock; systemic inflammatory response syndrome; SIRS;
KW   hormonal dysfunction; cancer; atherosclerosis; wound;
KW   tissue regeneration; haemophilia; leukaemia; reperfusion injury;
KW   psoriasis; diabetes; h-TRAAK polypeptide #1.
XX
OS   Homo sapiens.
XX
PN   WO200153454-A2.
XX
PD   26-JUL-2001.
XX
PF   22-DEC-2000; 2000WO-US34983.
XX
PR   21-JAN-2000; 2000US-0488725.
PR   25-APR-2000; 2000US-0552317.
PR   20-JUN-2000; 2000US-0598042.
PR   19-JUL-2000; 2000US-0620312.
PR   31-AUG-2000; 2000US-0653450.
PR   04-DEC-2000; 2000US-0729739.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Yamazaki V,  Tang YT,  Liu C,  Zhou P,  Wang D,  Zhang J,  Ren F;
PI   Asundi V,  Drmanac RT;
XX
DR   WPI; 2001-442255/47.
DR   N-PSDB; AAS08652.
XX
PT   New G-protein-coupled receptor-like polypeptides and polynucleotides,
PT   useful for treating diseases of ophthalmic, neurological, immunological
PT   and nephritic systems and hormonal dysfunction, cancer, atherosclerosis
PT   and diabetes -
XX
PS   Claim 10; Page 203-208; 259pp; English.
XX
CC   The sequence represents a human G-protein coupled receptor (GPCR)-like
CC   protein, found to be homologous to human h-TRAAK polypeptide #1.
CC   The GPCR-like polypeptides and polynucleotides are useful for
CC   the treatment of diseases of ophthalmic, neurological (e.g Alzheimer's
CC   disease and Parkinson's disease, immunological (e.g HIV infection and
CC   candidiasis), autoimmune disorders (e.g multiple sclerosis, systemic
CC   lupus erythematosus and rheumatoid arthritis), platelet disorders (e.g
CC   thrombocytopaenia and aplastic anaemia), inflammatory disorders (e.g.
CC   septic shock and systemic inflammatory response syndrome, SIRS) and
CC   nephritic systems. They may also be used to treat hormonal dysfunction,
CC   cancer, atherosclerosis, wounds, tissue regeneration, haemophilia,
CC   leukaemias, reperfusion injury, psoriasis and diabetes. Numerous examples
CC   of each type of disorder are given in the specification. Anti-GPCR-like
CC   protein antibodies are useful for detecting or quantitating the
CC   polypeptide in tissue. The polypeptides can also be used as molecular
CC   weight markers and as a food supplement.
XX
SQ   Sequence   1314 AA;


  Query Match             29.4%;  Score 822.5;  DB 22;  Length 1314;
  Best Local Similarity   48.4%;  Pred. No. 2.9e-65;
  Matches  164;  Conservative   55;  Mismatches   87;  Indels   33;  Gaps    4;

Qy      25 PVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKTVVAIFVVV 84
           |  :|  | :|  |||                                |:  |::|:  :|
Db     521 pparplqagsgagpapg--------------------------ramrsttllallalv 552

Qy      85 VVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDADNAGV 144
           ::|||:| |||||||| |   :  :   : :||| | ||| |||  ||:   ||   |
Db     553 llylvsgalvfraleqpheqqaqrelgevrekflrahpcvsdqelgllikevadalggga 612

Qy     145 SPIGNSSNNSSH--WDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLFGF 202
           |  ||::|||  |||||||||:||:||||||||:|  |: |::||| ||: ||||||
Db     613 dpetnstsnsshsawdlgsafffsgtiittigygnvalrtdagrlfcifyalvgiplfgi 672

Qy     203 LLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIFKY 262
           ||||:||:||:     |  :| :| |  |    :||:| :||:| ||::||  |  :| |
Db     673 llagvgdrlgsslrhgighieaiflkwhvppelvrvlsamlflligcllfvltptfvfcy 732

Qy     263 IEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVLSM 322
           :| |: ||:||||:|||||||||:||| :   :    |:|||||||:||||||:||:
Db     733 medwskleaiyfivtlttvgfgdyvagadprqd-spayqplvwfwillglayfasvltt 791

Qy     323 IGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRR 361
           ||:||||:|::|: |:| : | || |   |||  | |:|
Db     792 ignwlrvvsrrtraemggltaqaaswtgtvta--rvtqr 828


Search completed: September 21, 2002, 09:48:16
Job time: 4507 sec
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OM protein - protein search, using sw model

Run on: September 21, 2002, 08:36:04 ; Search time 32.67 Seconds
(without alignments)
405.972 Million cell updates/sec

Title: US-09-729-920-2
Perfect score: 2795
Sequence: 1 MKFPIETPRKQVNWDPKVAV.....IPTDTKDREPENNSLLEDRN 543

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1248.5	44.7	411	4	US-09-236-080-6	Sequence 6, Appli
2	1242.5	44.5	411	4	US-09-236-080-2	Sequence 2, Appli
3	1238.5	44.3	370	4	US-09-144-914-8	Sequence 8, Appli
4	447	16.0	107	4	US-09-236-080-4	Sequence 4, Appli
5	403	14.4	336	3	US-08-749-816-2	Sequence 2, Appli
6	403	14.4	336	4	US-09-144-914-2	Sequence 2, Appli
7	352.5	12.6	405	4	US-09-144-914-5	Sequence 5, Appli
8	349.5	12.5	394	4	US-09-144-914-4	Sequence 4, Appli
9	290.5	10.4	618	1	US-08-332-312-2	Sequence 2, Appli
10	212.5	7.6	336	1	US-08-332-312-4	Sequence 4, Appli
11	164.5	5.9	347	3	US-08-749-816-3	Sequence 3, Appli
12	164.5	5.9	347	4	US-09-144-914-6	Sequence 6, Appli
13	159	5.7	383	3	US-08-749-816-4	Sequence 4, Appli
14	159	5.7	383	4	US-09-144-914-7	Sequence 7, Appli
15	121.5	4.3	676	4	US-09-135-021-2	Sequence 2, Appli
16	121.5	4.3	676	4	US-09-135-020-2	Sequence 2, Appli
17	121.5	4.3	676	4	US-09-135-010A-2	Sequence 2, Appli
18	121.5	4.3	676	4	US-09-634-920-2	Sequence 2, Appli
19	113.5	4.1	1036	2	US-08-720-484A-5	Sequence 5, Appli
20	113.5	4.1	1036	4	US-08-953-823A-5	Sequence 5, Appli
21	110	3.9	754	4	US-09-214-564A-2	Sequence 2, Appli
22	109	3.9	680	1	US-07-674-287B-2	Sequence 2, Appli
23	109	3.9	680	2	US-08-436-900A-2	Sequence 2, Appli
24	105.5	3.8	473	1	US-08-597-236-13	Sequence 13, Appl
25	105.5	3.8	473	1	US-08-746-682A-13	Sequence 13, Appl
26	105.5	3.8	1312	2	US-08-592-126-148	Sequence 148, App
27	105.5	3.8	1312	2	US-08-687-080-51	Sequence 51, Appl
28	104.5	3.7	2509	2	US-08-149-097D-35	Sequence 35, Appl
29	103.5	3.7	376	4	US-09-135-020-113	Sequence 113, App
30	103.5	3.7	376	4	US-09-135-010A-113	Sequence 113, App
31	101	3.6	776	1	US-08-021-601-2	Sequence 2, Appli
32	101	3.6	776	1	US-08-082-849B-2	Sequence 2, Appli
33	101	3.6	776	5	PCT-US94-01624-2	Sequence 2, Appli
34	101	3.6	783	2	US-08-922-837-2	Sequence 2, Appli
35	101	3.6	783	4	US-09-351-550-2	Sequence 2, Appli
36	100.5	3.6	831	2	US-08-677-734A-11	Sequence 11, Appl
37	100.5	3.6	2336	4	US-09-268-163-10	Sequence 10, Appl
38	100	3.6	1388	4	US-09-572-191-2	Sequence 2, Appli
39	99.5	3.6	682	2	US-08-436-900A-4	Sequence 4, Appli
40	99.5	3.6	955	1	US-08-006-676B-1	Sequence 1, Appli
41	99.5	3.6	955	1	US-08-282-845-2	Sequence 2, Appli
42	99.5	3.6	955	5	PCT-US94-00324-1	Sequence 1, Appli
43	98.5	3.5	2265	2	US-08-149-097D-36	Sequence 36, Appl
44	97.5	3.5	664	1	US-08-421-661-6	Sequence 6, Appli
45	97.5	3.5	1093	4	US-09-315-793-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1
US-09-236-080-6
; Sequence 6, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217el Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236,080
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-236-080-6

Query Match 44.7%; Score 1248.5; DB 4; Length 411;
Best Local Similarity 64.3%; Pred. No. 1.2e-105;
Matches 247; Conservative 53; Mismatches 67; Indels 17; Gaps 5;

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Qy      22 AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI 80
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Db       2 AAPDLLDPKSA--------AQNSKPRLSFSSKPTVLASRVESDS---AINVMKWKTVSTI 50

Qy      81 FVVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD 140
           |:|||:||: |  ||:||||| | ||: || ::|  |:  | ||:  ||: ||| : |
Db      51 FLVVVLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAI 110

Qy     141 NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF 200
           |||: |:|||||  |||||||:||||||||||||:|||:| |||||||||:||: |||||
Db     111 NAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLF 170

Qy     201 GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF 260
           ||||||:|||||||||| ||:||  | |  |||||||:||||:||| ||::|| :|||||
Db     171 GFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIF 230

Qy     261 KYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL 320
           |:||||:||::|||||:||||:||||:|||| : | | ::|||:||||||||||||||||
Db     231 KHIEGWSALDAIYFVVITLTTIGFGDYVAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVL 289

Qy     321 SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM 380
           |||||||||:|||||||||| :|||||| |||||||:||||||||||:|| ||| ::
Db     290 SMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSV--- 346

Qy     381 ERRRLGLDQRAHSLDMLSPEKRSV 404
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Db    347 -KRKLSAELAGNHNQELTPCMRTL 369


RESULT   2
US-09-236-080-2
; Sequence 2, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
;  APPLICANT: Helen Meadows
;  APPLICANT: Conrad Chapman
;  TITLE OF INVENTION: No. 6242217el Compounds
;  FILE REFERENCE: GP30031
;  CURRENT APPLICATION NUMBER: US/09/236,080
;  CURRENT FILING DATE: 1999-01-25
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 411
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-236-080-2


  Query Match             44.5%;  Score 1242.5;  DB 4;  Length 411;
  Best Local Similarity   63.5%;  Pred. No. 4.2e-105;
  Matches  244;  Conservative   57;  Mismatches   66;  Indels   17;  Gaps    5;

Qy      22 AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI 80
           ||  :  ||||         |    |||| |:: ||:| |:|  :      |||||||  |
Db       2 AAPDLLDPKSA--------AQNSKPRLSFSTKPTVLASRVESDT---TINVMKWKTVSTI 50

Qy      81 FVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD 140
           |:|||:||: |  ||:||||| | ||: || ::|  |:  | ||:  ||: |||  : |
Db      51 FLVVVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAI 110

Qy     141 NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF 200
           |||: |:||:||  |||||||:||||||||||||:|||:| |||||||||:||: ||||
Db     111 NAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLF 170

Qy     201 GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF 260
           ||||||:|||||||||| ||:||  | |  |||||||:||||:||| ||::|| :||:||
Db     171 GFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIF 230

Qy     261 KYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL 320
           |:||||:||::|||||:||||:||||:|||| : | | ::|||:|||||||||||||||
Db     231 KHIEGWSALDAIYFVVITLTTIGFGDYVAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVL 289

Qy     321 SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM 380
           |||||||||:|||||||| :|||||| |||||||:|||||||||:|| ||| :|
Db     290 SMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSI--- 346

Qy     381 ERRRLGLDQRAHSLDMLSPEKRSV 404
           :|:|  :   :    |:| :|::
Db     347 -KRKLSAELAGNHNQELTPCRRTL 369


RESULT   3
US-09-144-914-8
; Sequence 8, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
;  APPLICANT: Duprat, Fabrice
;  APPLICANT: Lesage, Florian
;  APPLICANT: Fink, Michel
;  APPLICANT: Lazdunski, Michel
;  TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
;  TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
;  FILE REFERENCE: 989.6705CIP
;  CURRENT APPLICATION NUMBER: US/09/144,914
;  CURRENT FILING DATE: 1998-09-01
;  EARLIER APPLICATION NUMBER: 08/749,816
;  EARLIER FILING DATE: 1996-11-15
;  EARLIER APPLICATION NUMBER: 60/095,234
;  EARLIER FILING DATE: 1998-08-04
;  EARLIER APPLICATION NUMBER: FR 96/01565
;  EARLIER FILING DATE: 1996-02-08
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 370
;   TYPE: PRT
;   ORGANISM: Murine
;   FEATURE:
;   OTHER INFORMATION: TREK-1
US-09-144-914-8


  Query Match             44.3%;  Score 1238.5;  DB 4;  Length 370;
  Best Local Similarity   64.2%;  Pred. No. 8.3e-105;
  Matches  246;  Conservative   52;  Mismatches   68;  Indels   17;  Gaps    5;

Qy      22 AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI 80
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Db       2 AAPDLLDPKSA--------AQNSKPRLSFSSKPTVLASRVESDS---AINVMKWKTVSTI 50

Qy      81 FVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD 140
           |:|||:||: |  ||:||||| | ||: || ::|  |:  | ||:  ||: |||  : |
Db      51 FLVVVLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAI 110

Qy     141 NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF 200
           |||: |:||||  |||||||:||||||||||||:|||:| |||||||||:||: ||||
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Qy     201 GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF 260
           ||||||:|||||||||| ||:||  | |  |||||||:||||:||| ||::|| :||:||
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Qy     261 KYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL 320
           |:||||:||::|||||:||||:||||:|||| : | | ::|||:|||||||||||||||
Db     231 KHIEGWSALDAIYFVVITLTTIGFGDYVAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVL 289

Qy     321 SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM 380
           |||||||||:|||||||| :|||||| |||||||:|||||||||:|| ||| ::
Db     290 SMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSV--- 346

Qy     381 ERRRLGLDQRAHSLDMLSPEKRS 403
           :|:|  :   :    |:| |:
Db     347 -KRKLSAELAGNHNQELTPCMRT 368


RESULT   4
US-09-236-080-4
; Sequence 4, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
;  APPLICANT: Helen Meadows
;  APPLICANT: Conrad Chapman
;  TITLE OF INVENTION: No. 6242217el Compounds
;  FILE REFERENCE: GP30031
;  CURRENT APPLICATION NUMBER: US/09/236,080
;  CURRENT FILING DATE: 1999-01-25
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 107
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-236-080-4


  Query Match             16.0%;  Score 447;  DB 4;  Length 107;
  Best Local Similarity   77.6%;  Pred. No. 2e-33;
  Matches   83;  Conservative   12;  Mismatches   12;  Indels    0;  Gaps    0;

Qy     149 NSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLFGFLLAGIG 208
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Qy    209 DQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTI 255
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Db     61 DQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVAL 107


RESULT   5
US-08-749-816-2
; Sequence 2, Application US/08749816
; Patent No. 6013470
;  GENERAL INFORMATION:
;    APPLICANT:  Lesage, Florian
;    APPLICANT:  Guillemare, Eric
;    APPLICANT:  Fink, Michel
;    APPLICANT:  Duprat, Fabrice
;    APPLICANT:  Lazdunki, Michel
;    APPLICANT:  Romey, Georges
;    APPLICANT:  Barhanin, Jacques
;    TITLE OF INVENTION:  FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
;    TITLE OF INVENTION:  THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
;    TITLE OF INVENTION:  OF DRUGS
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  WEISER & ASSOCIATES
;      STREET:  230 South Fifteenth Street, Suite 500
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/749,816
;      FILING DATE:  15-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weiser, Gerard J.
;      REGISTRATION NUMBER:  19,763
;      REFERENCE/DOCKET NUMBER:  989.6351P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-875-8383
;      TELEFAX:  215-875-8394
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  336 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-749-816-2


  Query Match             14.4%;  Score 403;  DB 3;  Length 336;
  Best Local Similarity   33.2%;  Pred. No. 1.2e-28;
  Matches   95;  Conservative   53;  Mismatches  104;  Indels   34;  Gaps    9;

Qy      81 FVVV--VVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALD 138
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Db      25 FLVLGYLLYLVFGAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEQQLEQFLGRVLE 84

Qy     139 ADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIP 198
           | | ||| : |:| |  :||  || ||| ||::| |||:  | ::||| |||:|:: |||
Db      85 ASNYGVSVLSNASGN-WNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIP 143

Qy     199 LFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQV---------SQTKIRVISTIL--FILA 247
                |  :           : |:     :: |         |:  : ::  :|  |:
Db     144 FTLLFLTAV-----------VQRITVHVTRRPVLYFHIRWGFSKQVVAIVHAVLLGFVTV 192

Qy     248 GCIVFVTIPAVIFKYIE-GWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVW 306
           |  |  ||| :|  :|  |  ||| ||  ::|:|:| ||:| |      :|| ||  :
Db     193 SCFFF--IPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYKIGIT 250

Qy     307 FWILVGLAYFAAVLSMIGDWLRVLSK-----KTKEEVGEIKAHAAE 347
           ::|:||     ||    : |  | |       |::  | : |  |
Db     251 CYLLLGLIAMLVVLETFCE-LHELKKFRKMFYVKKDKDEDQVHIIE 295


RESULT   6
US-09-144-914-2
; Sequence 2, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
;  APPLICANT: Duprat, Fabrice
;  APPLICANT: Lesage, Florian
;  APPLICANT: Fink, Michel
;  APPLICANT: Lazdunski, Michel
;  TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
;  TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
;  FILE REFERENCE: 989.6705CIP
;  CURRENT APPLICATION NUMBER: US/09/144,914
;  CURRENT FILING DATE: 1998-09-01
;  EARLIER APPLICATION NUMBER: 08/749,816
;  EARLIER FILING DATE: 1996-11-15
;  EARLIER APPLICATION NUMBER: 60/095,234
;  EARLIER FILING DATE: 1998-08-04
;  EARLIER APPLICATION NUMBER: FR 96/01565
;  EARLIER FILING DATE: 1996-02-08
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 336
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: TWIK-1
US-09-144-914-2


  Query Match             14.4%;  Score 403;  DB 4;  Length 336;
  Best Local Similarity   33.2%;  Pred. No. 1.2e-28;
  Matches   95;  Conservative   53;  Mismatches  104;  Indels   34;  Gaps    9;

Qy      81 FVVV--VVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALD 138
           |:|:  ::||| | :|| ::| |:|    :  :    |  || :| |:| |:||  :   |:
Db      25 FLVLGYLLYLVFGAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEQQLEQFLGRVLE 84

Qy     139 ADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIP 198
           | | ||| : |:| |  :||  || ||| ||::| |||:  | ::||| |||:|:: |||
Db      85 ASNYGVSVLSNASGN-WNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIP 143

Qy     199 LFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQV---------SQTKIRVISTIL--FILA 247
                |  :           : |:     :: |         |:  : ::  :|  |:
Db     144 FTLLFLTAV-----------VQRITVHVTRRPVLYFHIRWGFSKQVVAIVHAVLLGFVTV 192

Qy     248 GCIVFVTIPAVIFKYIE-GWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVW 306
           |  |  ||| :|  :|  |  ||| ||  ::|:|:| ||:| |      :|| ||  :
Db     193 SCFFF--IPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYKIGIT 250

Qy     307 FWILVGLAYFAAVLSMIGDWLRVLSK-----KTKEEVGEIKAHAAE 347
           ::|:||     ||    : |  | |       |::  | : |  |
Db     251 CYLLLGLIAMLVVLETFCE-LHELKKFRKMFYVKKDKDEDQVHIIE 295


RESULT   7
US-09-144-914-5
; Sequence 5, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
;  APPLICANT: Duprat, Fabrice
;  APPLICANT: Lesage, Florian
;  APPLICANT: Fink, Michel
;  APPLICANT: Lazdunski, Michel
;  TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
```

```
;  TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
;  FILE REFERENCE: 989.6705CIP
;  CURRENT APPLICATION NUMBER: US/09/144,914
;  CURRENT FILING DATE: 1998-09-01
;  EARLIER APPLICATION NUMBER: 08/749,816
;  EARLIER FILING DATE: 1996-11-15
;  EARLIER APPLICATION NUMBER: 60/095,234
;  EARLIER FILING DATE: 1998-08-04
;  EARLIER APPLICATION NUMBER: FR 96/01565
;  EARLIER FILING DATE: 1996-02-08
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 405
;   TYPE: PRT
;   ORGANISM: Murine
;   FEATURE:
;   OTHER INFORMATION: TASK
US-09-144-914-5


  Query Match             12.6%;  Score 352.5;  DB 4;  Length 405;
  Best Local Similarity   32.1%;  Pred. No. 6.5e-24;
  Matches   90;  Conservative   53;  Mismatches  110;  Indels   27;  Gaps    8;

Qy      78 VAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSP---QELETLIQ 134
           :|: |    ||: |  || |||   |  ::  : | : | ||    :|    :||| ::
Db       6 LALIVCTFTYLLVGAAVFDALESEPEMIERQRLELRQLE-LRARYNLSEGGYEELERVVL 64

Qy     135 HALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAI 194
             |    |||            |    :|:|| |||||||||: |||||:|||:||: ||:
Db      65 R-LKPHKAGV----------QWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYAL 112

Qy     195 FGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVT 254
           ||||   :   :|::: |     : | :   |   :   :: : : :|     ||  :
Db     113 LGIPLTLIMFQSLGERINTFVRYLLHRAK---RGLGMRHAEVSMANMVLIGFVSCISTLC 169

Qy     255 IPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVA-GGNAGINYREWYKPLVWFWILVGL 313
           | |  | | | ||  :: |:  :||||:||||:||   :  :  :  |    : :|| ||
Db     170 IGAAAFSYYERWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYIILTGL 229

Qy     314 AYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVT 353
             | |:::   || ::   ::|  :     || :| :|
Db     230 TVIGAFLNLV--VLRFMTMNAEDEKRD-----AEHRALLT 262


RESULT   8
US-09-144-914-4
; Sequence 4, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
;  APPLICANT: Duprat, Fabrice
;  APPLICANT: Lesage, Florian
;  APPLICANT: Fink, Michel
;  APPLICANT: Lazdunski, Michel
;  TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
;  TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
;  FILE REFERENCE: 989.6705CIP
;  CURRENT APPLICATION NUMBER: US/09/144,914
;  CURRENT FILING DATE: 1998-09-01
;  EARLIER APPLICATION NUMBER: 08/749,816
;  EARLIER FILING DATE: 1996-11-15
;  EARLIER APPLICATION NUMBER: 60/095,234
;  EARLIER FILING DATE: 1998-08-04
;  EARLIER APPLICATION NUMBER: FR 96/01565
;  EARLIER FILING DATE: 1996-02-08
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 394
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: TASK
US-09-144-914-4


  Query Match             12.5%;  Score 349.5;  DB 4;  Length 394;
  Best Local Similarity   32.8%;  Pred. No. 1.2e-23;
  Matches   95;  Conservative   53;  Mismatches  109;  Indels   33;  Gaps   10;

Qy      72 MKWKTV--VAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSP--- 126
           || : |  :|: |    ||: |  || |||   |  ::  : | : | ||    :|
Db       1 MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQE-LRARYNLSQGGY 59

Qy     127 QELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGK 186
           :||| ::   |    |||           |    :|:|| |||||||||: ||||:|||
Db      60 EELERVVLR-LKPHKAGV----------QWRFAGSFYFAITVITTIGYGHAAPSTDGGK 107

Qy     187 IFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEK--VFRKKQVSQTKIRVISTILF 244
           :||: ||: ||||   :   :|::: |:    : | :|    |:  ||   :     :|
Db     108 VFCMFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANM-----VLI 162

Qy     245 ILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVA-GGNAGINYREWYKP 303
             ||  : | |  | : | ||  :: |:  :||||:||||:||   :  :  :  |
Db     163 GFFSCISTLCIGAAAFSHYEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVA 222

Qy     304 LVWFWILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVT 353
             : :|| ||    | |:::   || ::   ::|  :     || :| :|
Db     223 FSFVYILTGLTVIGAFLNLV--VLRFMTMNAEDEKRD-----AEHRALLT 265


RESULT   9
US-08-332-312-2
; Sequence 2, Application US/08332312
; Patent No. 5559026
;  GENERAL INFORMATION:
;    APPLICANT:  Price, Laura A.
;    APPLICANT:  Pausch, Mark H.
;    TITLE OF INVENTION:  Functional Expression of a Drosphila
;    TITLE OF INVENTION:  Melanagaster Putative Potassium Channel in Yeast
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  American Cyanamid Company
;      STREET:  One Cyanamid Plaza
;      CITY:  Wayne
;      STATE:  New Jersey
;      COUNTRY:  US
;      ZIP:  07470-8426
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/332,312
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Harrington, James J.
;      REGISTRATION NUMBER:  P-38,711
;      REFERENCE/DOCKET NUMBER:  32,421
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-831-3246
;      TELEFAX:  201-831-3305
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  618 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-332-312-2


  Query Match             10.4%;  Score 290.5;  DB 1;  Length 618;
  Best Local Similarity   23.6%;  Pred. No. 5.6e-18;
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  Matches  113;  Conservative   88;  Mismatches  181;  Indels   97;  Gaps   20;

Qy      73 KWKTVVAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETL 132
           :|   : : :  : ||: |  ::  :|   |        : :||  :  : ::   || |
Db       5 RW---ILLLIFYISYLMFGAAIYYHIEHGEEK-------ISRAEQRKAQIAINEYLLEEL 54

Qy     133 ----------IQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPS 181
                    :|   |  :  |:       :    |    ||||| || :|:|||||:|:
Db      55 GDKNTTTQDEILQRISDYCDKPVTLPPTYDDTPYTWTFYHAFFFAFTVCSTVGYGNISPT 114

Qy     182 TEGGKIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVS------QTK 235
           |  |::  | |:: |||: | | ||:|:     ||::   : : ::| ::|        :
Db     115 TFAGRMIMIAYSVIGIPVNGILFAGLGE----YFGRTFEAIYRRYKKYKMSTDMHYVPPQ 170

Qy     236 IRVISTILF-ILAGCIVFVTIPAVIFKYIE--GWTALESIYFVVVTLTTVGFGDFVA--G 290
           : :|:|::  :: |  :|: :| |    :   | ::: |:|:  || ||:||||:|   |
Db     171 LGLITTVVIALIPGIALFLVLPCVGVHLLRELGLSSI-SLYYSYVTTTTIGFGDYVPTFG 229

Qy     291 GNAGINYREW---YKPLVWFWILVGLAYFAAVLSMIGDWLRVLSKK----TKEEVGEIKA 343
             |    :  |   |:  |  | : | |   ::: |   |:  |||     ::    :||
Db     230 ANQPKEFGGWFVVYQIFVIVWFIFSLGYLVMIMTFITRGLQ--SKKLAYLEQQLSSNLKA 287

Qy     344 HAAEWKANVTAEFRETRRRLS-------------VEIHDKLQRAATIRSMERRR-----L 385
                 : || :    || |:              |:|   | |: :   :   |     :
Db     288 TQNRIWSGVTKDVGYLRRMLNELYILKVKPVYTDVDIAYTLPRSNSCPDLSMYRVEPAPI 347

Qy     386 GLDQRAHSL--DMLSPEKRS--VFAALDTGRFKASSQESINNRP-------------NNL 428
              :|| |:  ||:  :: :  | |  ||   |   :::                 | |
Db     348 PSRKRAFSVCADMVGAQREAGMVHANSDTDLTKLDREKTFETAEAYHQTTDLLAKVVNAL 407

Qy     429 RLKGP-----EQLNKHG--QGASEDNI---------INKFGSTSRLTKRKNKDLKKTLP 471
               |     |    :|   | |:  |          :|:| |  |   |   |     |
Db     408 ATVKPPPAEQEDAALYGGYHGFSDSQILASEWSFSTVNEFTSPRRPRARACSDFNLEAP 466


RESULT  10
US-08-332-312-4
; Sequence 4, Application US/08332312
; Patent No. 5559026
;  GENERAL INFORMATION:
;    APPLICANT:  Price, Laura A.
;    APPLICANT:  Pausch, Mark H.
;    TITLE OF INVENTION:  Functional Expression of a Drosphila
;    TITLE OF INVENTION:  Melanagaster Putative Potassium Channel in Yeast
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  American Cyanamid Company
;      STREET:  One Cyanamid Plaza
;      CITY:  Wayne
;      STATE:  New Jersey
;      COUNTRY:  US
;      ZIP:  07470-8426
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/332,312
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Harrington, James J.
;      REGISTRATION NUMBER:  P-38,711
;      REFERENCE/DOCKET NUMBER:  32,421
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-831-3246
;      TELEFAX:  201-831-3305
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  336 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-332-312-4


  Query Match             7.6%;  Score 212.5;  DB 1;  Length 336;
  Best Local Similarity   29.2%;  Pred. No. 2.9e-11;
  Matches   54;  Conservative   29;  Mismatches   59;  Indels   43;  Gaps    5;

Qy     157 WDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLFGFLLAGIGDQLGTIFG 216
           |   |: ||| ||:|||||||  | |  |:|:|||::: ||||    |  | |  |
Db      28 WTFSSSIFFAVTVVTTIGYGNPVPVTNIGRIWCILFSLLGIPL---TLVTIADLAGKFLS 84

Qy     217 KS--------------IARVEKVFRK-------------KQVSQTKIRVISTILFILA 247
           :                ::|  |  |:               : : :|        :||
Db      85 EHLVWLYGNYLKLKYLILSRHRKERREHVCEHCHSHGMGHDMNIEEKRI----PAFLVLA 140

Qy     248 GCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWF 307
             ||:     |:   :| |:   | |:  :|:|||||||  :         |: |  ::
Db     141 ILIVYTAFGGVLMSKLEPWSFFTSFYWSFITMTTVGFGDLMP-------RRDGYMYIILL 193

Qy     308 WILVG 312
           :|::|
Db     194 YIILG 198


RESULT  11
US-08-749-816-3
; Sequence 3, Application US/08749816
; Patent No. 6013470
;  GENERAL INFORMATION:
;    APPLICANT:  Lesage, Florian
;    APPLICANT:  Guillemare, Eric
;    APPLICANT:  Fink, Michel
;    APPLICANT:  Duprat, Fabrice
;    APPLICANT:  Lazdunki, Michel
;    APPLICANT:  Romey, Georges
;    APPLICANT:  Barhanin, Jacques
;    TITLE OF INVENTION:  FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
;    TITLE OF INVENTION:  THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
;    TITLE OF INVENTION:  OF DRUGS
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  WEISER & ASSOCIATES
;      STREET:  230 South Fifteenth Street, Suite 500
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/749,816
;      FILING DATE:  15-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weiser, Gerard J.
;      REGISTRATION NUMBER:  19,763
;      REFERENCE/DOCKET NUMBER:  989.6351P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-875-8383
;      TELEFAX:  215-875-8394
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  347 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-749-816-3
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  Query Match             5.9%;  Score 164.5;  DB 3;  Length 347;
  Best Local Similarity   24.1%;  Pred. No. 7.2e-07;
  Matches   65;  Conservative   44;  Mismatches  116;  Indels   45;  Gaps    8;

Qy      54 ATVVARMEGTSQGGLQTVMKWKTVVAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALE 113
           :|:      | |   | |     : |   ::|  |:  |: : |  |
Db      17 STMQKMSPNTRQNFRQNVNVVVCLSAAITLLVFNLIGAGIFYLAETQ-----------N 64

Qy     114 KAEFLRDHVCVSPQELETLIQHALDADNAGVSPIGNSSNNSSHWD-LGSAFFFAGTVITT 172
           :| | ::  ||       |   : |:    | :|     ||  |  | | ||: |: :|
Db      65 SSESLNENSEVSKCLHNLPIGGKITAEMK--SKLGKCLTKSSRIDGFGKAIFFSWTLYST 122

Qy     173 IGYGNIAPSTEGGKIFCILYAIFGIPL-------FGFLLAGIGDQLGTIFGKSIARVEKV 225
           :|||:: | :  |:   | |::  ||:       ||  ||     |  :  ::   |:|
Db     123 VGYGSLYPHSTLGRYLTIFYSLLMIPVFIAFKFEFGTFLAHF---LVVVSNRTRLAVKKA 179

Qy     226 FRKKQVSQTKIRVIST------ILFI--LAGCIVFVTIPAVIFKYIEGWTALESIYFVVV 277
           : |   :       |       ::|:  |  | : :   : :|  ||  : | |:|| ::
Db     180 YYKLSQNPENAETPSNSLQHDYLIFLSSLLLCSISLLSSSALFSSIENISYLSSVYFGII 239

Qy     278 TLTTVGFGDFVAGGNAGINYREWYKPLVWF 307
           |:  :| || |               ||||
Db     240 TMFLIGIGDIVPTN-----------LVWF 257


RESULT  12
US-09-144-914-6
; Sequence 6, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
;  APPLICANT: Duprat, Fabrice
;  APPLICANT: Lesage, Florian
;  APPLICANT: Fink, Michel
;  APPLICANT: Lazdunski, Michel
;  TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
;  TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
;  FILE REFERENCE: 989.6705CIP
;  CURRENT APPLICATION NUMBER: US/09/144,914
;  CURRENT FILING DATE: 1998-09-01
;  EARLIER APPLICATION NUMBER: 08/749,816
;  EARLIER FILING DATE: 1996-11-15
;  EARLIER APPLICATION NUMBER: 60/095,234
;  EARLIER FILING DATE: 1998-08-04
;  EARLIER APPLICATION NUMBER: FR 96/01565
;  EARLIER FILING DATE: 1996-02-08
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 347
;   TYPE: PRT
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism: TWIK-1 homolog
US-09-144-914-6


  Query Match             5.9%;  Score 164.5;  DB 4;  Length 347;
  Best Local Similarity   24.1%;  Pred. No. 7.2e-07;
  Matches   65;  Conservative   44;  Mismatches  116;  Indels   45;  Gaps    8;

Qy      54 ATVVARMEGTSQGGLQTVMKWKTVVAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALE 113
           :|:      | |   | |     : |   ::|  |:  |: : |  |
Db      17 STMQKMSPNTRQNFRQNVNVVVCLSAAITLLVFNLIGAGIFYLAETQ-----------N 64

Qy     114 KAEFLRDHVCVSPQELETLIQHALDADNAGVSPIGNSSNNSSHWD-LGSAFFFAGTVITT 172
           :| | ::  ||       |   : |:    | :|     ||  |  | | ||: |: :|
Db      65 SSESLNENSEVSKCLHNLPIGGKITAEMK--SKLGKCLTKSSRIDGFGKAIFFSWTLYST 122

Qy     173 IGYGNIAPSTEGGKIFCILYAIFGIPL-------FGFLLAGIGDQLGTIFGKSIARVEKV 225
           :|||:: | :  |:   | |::  ||:       ||  ||     |  :  ::   |:|
Db     123 VGYGSLYPHSTLGRYLTIFYSLLMIPVFIAFKFEFGTFLAHF---LVVVSNRTRLAVKKA 179

Qy     226 FRKKQVSQTKIRVIST------ILFI--LAGCIVFVTIPAVIFKYIEGWTALESIYFVVV 277
           : |   :       |       ::|:  |  | : :   : :|  ||  : | |:|| ::
Db     180 YYKLSQNPENAETPSNSLQHDYLIFLSSLLLCSISLLSSSALFSSIENISYLSSVYFGII 239

Qy     278 TLTTVGFGDFVAGGNAGINYREWYKPLVWF 307
           |:  :| || |               ||||
Db     240 TMFLIGIGDIVPTN-----------LVWF 257


RESULT  13
US-08-749-816-4
; Sequence 4, Application US/08749816
; Patent No. 6013470
;  GENERAL INFORMATION:
;    APPLICANT:  Lesage, Florian
;    APPLICANT:  Guillemare, Eric
;    APPLICANT:  Fink, Michel
;    APPLICANT:  Duprat, Fabrice
;    APPLICANT:  Lazdunki, Michel
;    APPLICANT:  Romey, Georges
;    APPLICANT:  Barhanin, Jacques
;    TITLE OF INVENTION:  FAMILY OF MAMMALIAN POTASSIUM CHANNELS,
;    TITLE OF INVENTION:  THEIR CLONING AND THEIR USE ESPECIALLY FOR THE SCREENING
;    TITLE OF INVENTION:  OF DRUGS
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  WEISER & ASSOCIATES
;      STREET:  230 South Fifteenth Street, Suite 500
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19102
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/749,816
;      FILING DATE:  15-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Weiser, Gerard J.
;      REGISTRATION NUMBER:  19,763
;      REFERENCE/DOCKET NUMBER:  989.6351P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-875-8383
;      TELEFAX:  215-875-8394
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  383 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-749-816-4


  Query Match             5.7%;  Score 159;  DB 3;  Length 383;
  Best Local Similarity   22.1%;  Pred. No. 2.7e-06;
  Matches   85;  Conservative   57;  Mismatches  154;  Indels   88;  Gaps   16;

Qy      85 VVYLVTGGLVFRALEQPFESSQKNTIALE----KAEF---LRDHVCVSPQELE----TLI 133
           | | : |  :| ::| | |  ::      |    | :|   :   :  | | :|     ||
Db      49 VTYALGGAYLFLSIEHPEELKRREKAIREFQDLKQQFMGNITSGIENSEQSIEIYTKKLI 108

Qy     134 QHALDADNAGVSP--IGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCIL 191
           || ||        |       |   ||  |  | :  :||| | | :  |::  |
Db     109 LMLEDAHNAHAFEYFFLNHEIPKDMWTFSSALVFTTTTVIPVGYGYIFPVSAYGRMCLIA 168

Qy     192 YAIFGIPLFGFLLAGIGDQLGTIFGKSIAR-VEKVFRKKQVSQTKIRVISTILFILAGCI 250
           ||: ||||    |  : |      ||  |: | : |    ::      |   :|:   |:
Db     169 YALLGIPL---TLVTMADT-----GKFAAQLVTRWFGDNNMA------IPAAIFV---CL 211
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Qy    251 VFV--TIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFW 308
          :|    :   |       | |:|:|| : :: |:|||     |
Db    212 LFAYPLVVGFILCSTSNITYLDSVYFSLTSIFTIGFGDLTPDMN---------------- 255

Qy    309 ILVGLAYFAAV-LSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEI 367
           :: :  | || : ::   | ::: :  : | :  |  : |                  |:
Db    256 -VIHMVLFLAVGVILVTITLDIVAAEMIDRVHYMGRHVGKAK---------------EL 298

Qy    368 HDKLQRAATIRSMER-----------RRLGLDQRAHSLD--------MLSPEKRSVFAA 407
            |: : |   :|::             | |:      :|          ||:
Db    299 AGKMFQLAQSLNMKQGLVSGVGQLHALARFGMLVGREEVDKTQEDGIIAFSPDVMDGLEF 358

Qy    408 LDT-GRFKASSQESINNRPNNLRL 430
          :||   :   |: |  |   || |
Db    359 MDTLSIYSRRSRRSAENSARNLFL 382


RESULT 14
US-09-144-914-7
; Sequence 7, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
;  APPLICANT: Duprat, Fabrice
;  APPLICANT: Lesage, Florian
;  APPLICANT: Fink, Michel
;  APPLICANT: Lazdunski, Michel
;  TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
;  TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
;  FILE REFERENCE: 989.6705CIP
;  CURRENT APPLICATION NUMBER: US/09/144,914
;  CURRENT FILING DATE: 1998-09-01
;  EARLIER APPLICATION NUMBER: 08/749,816
;  EARLIER FILING DATE: 1996-11-15
;  EARLIER APPLICATION NUMBER: 60/095,234
;  EARLIER FILING DATE: 1998-08-04
;  EARLIER APPLICATION NUMBER: FR 96/01565
;  EARLIER FILING DATE: 1996-02-08
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 383
;   TYPE: PRT
;   ORGANISM: Unknown
;   FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism: TWIK-1 homolog
US-09-144-914-7


  Query Match             5.7%;  Score 159;  DB 4;  Length 383;
  Best Local Similarity   22.1%;  Pred. No. 2.7e-06;
  Matches   85;  Conservative   57;  Mismatches  154;  Indels   88;  Gaps   16;

Qy     85 VVYLVTGGLVFRALEQPFESSQKNTIALE----KAEF---LRDHVCVSPQELE----TLI 133
          | | : |  :| ::| | |   ::     |    | :|   :   :  | | :|     ||
Db     49 VTYALGGAYLFLSIEHPEELKRREKAIREFQDLKQQFMGNITSGIENSEQSIEIYTKKLI 108

Qy    134 QHALDADNAGVSP--IGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCIL 191
              || ||        |       |   ||  |  | :  :|||  | |  :  |::  |
Db    109 LMLEDAHNAHAFEYFFLNHEIPKDMWTFSSALVFTTTTVIPVGYGYIFPVSAYGRMCLIA 168

Qy    192 YAIFGIPLFGFLLAGIGDQLGTIFGKSIAR-VEKVFRKKQVSQTKIRVISTILFILAGCI 250
          ||: ||||    |  : |      ||  |: | : |    ::       |   :|:   |:
Db    169 YALLGIPL---TLVTMADT-----GKFAAQLVTRWFGDNNMA------IPAAIFV---CL 211

Qy    251 VFV--TIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFW 308
          :|    :   |       | |:|:|| : :: |:|||     |
Db    212 LFAYPLVVGFILCSTSNITYLDSVYFSLTSIFTIGFGDLTPDMN---------------- 255

Qy    309 ILVGLAYFAAV-LSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEI 367
           :: :  | || : ::   | ::: :  : | :  |  : |                  |:
Db    256 -VIHMVLFLAVGVILVTITLDIVAAEMIDRVHYMGRHVGKAK---------------EL 298

Qy    368 HDKLQRAATIRSMER-----------RRLGLDQRAHSLD--------MLSPEKRSVFAA 407
            |: : |   :|::             | |:      :|          ||:
Db    299 AGKMFQLAQSLNMKQGLVSGVGQLHALARFGMLVGREEVDKTQEDGIIAFSPDVMDGLEF 358

Qy    408 LDT-GRFKASSQESINNRPNNLRL 430
          :||   :   |: |  |   || |
Db    359 MDTLSIYSRRSRRSAENSARNLFL 382


RESULT 15
US-09-135-021-2
; Sequence 2, Application US/09135021A
; Patent No. 6150104
; GENERAL INFORMATION:
;  APPLICANT: Splawski, Igor
;  APPLICANT: Keating, Mark T.
;  TITLE OF INVENTION: A HOMOZYGOUS MUTATION IN KVLQT1 WHICH CAUSES JERVELL
;  TITLE OF INVENTION: AND LANGE-NIELSEN SYNDROME
;  FILE REFERENCE: 2323-128
;  CURRENT APPLICATION NUMBER: US/09/135,021A
;  CURRENT FILING DATE: 1998-08-17
;  EARLIER APPLICATION NUMBER: 08/874,655
;  EARLIER FILING DATE: 1997-06-13
;  EARLIER APPLICATION NUMBER: 60/094,477
;  EARLIER FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 80
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 676
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-135-021-2


  Query Match             4.3%;  Score 121.5;  DB 4;  Length 676;
  Best Local Similarity   19.4%;  Pred. No. 0.017;
  Matches  120;  Conservative  108;  Mismatches  229;  Indels  163;  Gaps   32;

Qy     16 PKVAVPA--AAPVCQPKSATNGQPPAPAPTPTPRLSI-SSRATVVAR--MEGTSQGGLQT 70
          |  | ||  |||   | ::  |  | |  :  ||:|| |:|  |:||  ::|     |:
Db     59 PGPAPPASPAAPAAPPVASDLG--PRPPVSLDPRVSIYSTRRPVLARTHVQGRVYNFLER 116

Qy     71 VMKWKTVV---AIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQ 127
             ||  |   |:|::|:| |:    |   :|| : :   |:      |  : | |
Db    117 PTGWKCFVYHFAVFLIVLVCLIFS--VLSTIEQ-YAALATGTL------FWMEIVLVVFF 167

Qy    128 ELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPST----- 182
          | :::            : ::   | : |     ||   |: |    :  |
Db    168 GTEYVVR-----------LWSAGCRSKYVGLWGRLRFARKPISIIDLIVVVASMVVLCV 215

Qy    183 -EGGKIFCILYAIFGIPLFGFL-LAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVIS 240
           |::|    || ||     | :  :  | ||   : :  |  : |:: ::   |  :
Db    216 GSKGQVFA-TSAIRGIRFLQILRMLHVDRQGGT--WRLLGSVVFIHRQELITTLYIGFLG 272

Qy    241 TILFILAGCIVFVTIPAVIFK--YIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYR 298
          | :   |::     : :   :|  :  ::::: |||:||:|:|| |          :
Db    273 ---LIFSSYFVYLAEKDAVNESGRVEFGSYADALWWGVVTVTTIGYGDKVP--------Q 321

Qy    299 EWY-KPLVWFWILVGLAYFAAVLSMIGDW--LRVLSKKTKEEVG-EIKAHAA----EWKA 350
          ~  | | :   : :  :::||    ::|    |:|  |: ::    :| | |:     |:
Db    322 TWVGKTIASCFSVFAISFFALPAGILGSGFALKVQQKQRQKHFNRQIPAAASLIQTAWRC 381

Qy    351 NVTAEFRETRRRLSVEIHDKLQRAATIRS---MERRRLGLDQRAHSLD----------ML 397
                :  :: :    |  |: |: |     :: : : ::   ||          ||
Db    382 YAAENPDSSTWKIYIR---KAPRSHTLLSPSPKPKKSVVVKKKKFKLDKDNGVTPGEKML 438

Qy    398 S--------PEKRSVFAALDTGRFKASSQE-SINNRPNNLRLKGP---------EQLNKH 439
          :        ||:| :         |    : |:   |  | :  |         | |:
Db    439 TVPHITCDPPEERRL------DHFSVDGYDSSVRKSPTLLEVSMPHFMRTNSFAEDLDLE 492

Qy    440 GQGASEDNIINKFGSTSRL-----------------TKRKNKDLKKTLPEDVQKIYKTF 481
          |     : ::      |:|                 |:|  :  :|  | ||: : : :
Db    493 G-----ETLLTPITHISQLREHHRATIKVIRRMQYFVAKKKFQQARK--PYDVRDVIEQY 545
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```
Qy     482 RN-------------------------YSLDEEKKE----------EETEKMCNSDNSS 505
                                       |: |: |:            |      :
Db     546 SQGHLNLMVRIKELQRRLDQSIGKPSLFISVSEKSKDRGSNTIGARLNRVEDKVTQLDQR 605

Qy     506 TAMLTDCIQQHAELENGMIP 525
           |::|| : |   |  |  |
Db     606 LALITDMLHQLLSLHGGSTP 625
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Search completed: September 21, 2002, 09:49:02
Job time: 4378 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: September 21, 2002, 08:38:29 ; Search time 49.26 Seconds
(without alignments)
1059.206 Million cell updates/sec

Title: US-09-729-920-2
Perfect score: 2795
Sequence: 1 MKFPIETPRKQVNWDPKVAV.....IPTDTKDREPENNSLLEDRN 543

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	403	14.4	336	2	S65566	inward rectifier p
2	329	11.8	330	2	JC7703	TASK-5 protein - h
3	326	11.7	1001	2	T13807	potassium channel
4	315.5	11.3	329	2	T43509	probable potassium
5	307	11.0	336	2	T32347	outward rectifier
6	300.5	10.8	364	2	T43361	probable potassium
7	298.5	10.7	393	2	T25392	hypothetical prote
8	294.5	10.5	1910	2	H88124	protein T12C9.3 [i
9	290.5	10.4	334	2	T19860	hypothetical prote
10	282.5	10.1	392	2	T45032	hypothetical prote
11	268.5	9.6	522	2	T24265	hypothetical prote
12	265.5	9.5	528	2	T21834	hypothetical prote
13	264.5	9.5	444	2	T26229	hypothetical prote
14	264	9.4	551	2	T16426	hypothetical prote
15	264	9.4	555	2	T43357	potassium channel
16	262.5	9.4	443	2	T21598	hypothetical prote
17	260	9.3	461	2	T43394	potassium channel
18	258.5	9.2	513	2	T28933	hypothetical prote
19	255	9.1	452	2	T21118	hypothetical prote
20	252.5	9.0	586	2	T21683	hypothetical prote
21	248	8.9	325	2	T15584	hypothetical prote
22	247	8.8	427	2	T27681	hypothetical prote
23	245	8.8	1136	2	T26953	hypothetical prote
24	244	8.7	504	2	T22269	hypothetical prote
25	233.5	8.4	484	2	T43529	probable potassium
26	233.5	8.4	519	2	T16629	hypothetical prote
27	233.5	8.4	1539	2	T30037	hypothetical prote
28	229.5	8.2	383	2	T23182	hypothetical prote
29	227.5	8.1	307	2	H89074	protein twk-24 [im
30	224.5	8.0	524	2	T23907	hypothetical prote
31	224.5	8.0	769	2	T27550	hypothetical prote
32	221.5	7.9	643	2	T26616	hypothetical prote
33	218	7.8	335	2	S44635	f22b7.7 protein -
34	217.5	7.8	691	2	S46585	outward-rectifier
35	216.5	7.7	576	2	T43363	potassium channel
36	213.5	7.6	660	2	T21551	hypothetical prote
37	213	7.6	569	2	T43531	probable potassium
38	210.5	7.5	544	2	T43364	potassium channel
39	208.5	7.5	485	2	T24201	hypothetical prote
40	207.5	7.4	700	2	T27364	hypothetical prote
41	204.5	7.3	550	2	T22557	hypothetical prote
42	203.5	7.3	539	2	T23700	hypothetical prote
43	202	7.2	681	2	T19429	hypothetical prote
44	198	7.1	631	2	T26232	hypothetical prote
45	189.5	6.8	475	2	T27725	hypothetical prote

ALIGNMENTS

RESULT 1
S65566
inward rectifier potassium channel TWIK-1 - human
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C;Accession: S65566
R;Lesage, F.; Guillemare, E.; Fink, M.; Duprat, F.; Lazdunski, M.; Romey, G.; Barhani
EMBO J. 15, 1004-1011, 1996
A;Title: TWIK-1, a ubiquitous human weakly inward rectifying K(+) channel with a nove
A;Reference number: S65566; MUID:96183184
A;Accession: S65566
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-336 <LES>
A;Cross-references: EMBL:U33632; NID:g1086490; PIDN:AAB01688.1; PID:g1086491

Query Match 14.4%; Score 403; DB 2; Length 336;
Best Local Similarity 33.2%; Pred. No. 1.2e-20;
Matches 95; Conservative 53; Mismatches 104; Indels 34; Gaps 9;

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Qy      81 FVVV--VVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALD 138
           |:|:  ::||| | :|| ::| |:|   :  :   |  || :| |:| |:||  :   |:
Db      25 FLVLGYLLYLVFGAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEQQLEQFLGRVLE 84

Qy     139 ADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIP 198
           | | ||| : |:| |  :||  || ||| ||::| |||:  | ::||| |||:|:: |||
Db      85 ASNYGVSVLSNASGN-WNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIP 143

Qy     199 LFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQV---------SQTKIRVISTIL--FILA 247
                |  :           : |:     :: |         |:  : ::  :|  |:
Db     144 FTLLFLTAV-----------VQRITVHVTRRPVLYFHIRWGFSKQVVAIVHAVLLGFVTV 192

Qy     248 GCIVFVTIPAVIFKYIE-GWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVW 306
           |  |  ||| :|  :|  |  ||| ||  ::|:|:| ||:| |      :|| ||  :
Db     193 SCFFF--IPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYKIGIT 250

Qy     307 FWILVGLAYFAAVLSMIGDWLRVLSK-----KTKEEVGEIKAHAAE 347
            ::|:||     ||    : |  | |       |::  | : |  |
Db     251 CYLLLGLIAMLVVLETFCE-LHELKKFRKMFYVKKDKDEDQVHIIE 295
```

RESULT 2
JC7703
TASK-5 protein - human
C;Species: Homo sapiens (man)
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: JC7703
R;Kim, D.; Gnatenco, C.
Biochem. Biophys. Res. Commun. 284, 923-930, 2001
A;Title: TASK-5, a new member of the tandem-pore K+ channel family.
A;Reference number: JC7703; MUID:21303050; PMID:11409881

A;Accession: JC7703
A;Molecule type: DNA
A;Residues: 1-330 <KIM>
A;Cross-references: GB:AL118522
C;Comment: This protein, a new member of the tandem-pore K+ channel family with four tra
hormone secretion, but does not produce a functional plasma membrane K+ current by itsel
C;Genetics:
A;Gene: task-5
A;Map position: 20q12
C;Keywords: transmembrane protein
F;7-30/Domain: transmembrane segment #status predicted <TMS1>
F;107-128/Domain: transmembrane segment #status predicted <TMS2>
F;129-155/Region: hydrophobic cytoplasmic linker #status predicted
F;156-180/Domain: transmembrane segment #status predicted <TMS3>
F;220-240/Domain: transmembrane segment #status predicted <TMS4>

Query Match 11.8%; Score 329; DB 2; Length 330;
Best Local Similarity 32.4%; Pred. No. 1.7e-15;
Matches 85; Conservative 46; Mismatches 97; Indels 34; Gaps 9;

Qy 80 IFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDA 139
Db 11 LVLCTLCYLLVGAAVFDALESEAESGRQR-LLVQKRGALRRKFGFSAEDYRELERLALQA 69

Qy 140 D--NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGI 197
Db 70 EPHRAG-----------RQWKFPGSFYFAITVITTIGYGHAAPGTDSGKVFCMFYALLGI 118

Qy 198 PLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAG---CIVFVT 254
Db 119 PLTLVTFQSLGERLNAV----VRRL--LLAAKCCLGLRWTCVSTENLVVAGLLACAATLA 172

Qy 255 IPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVA--GGNAGINYREWYKPLVWFWILVG 312
Db 173 LGAVAFSHFEGWTFFHAYYYCFITLTTIGFGDFVALQSGEA-LQRKLPYVAFSFLYILLG 231

Qy 313 LAYFAAVLSMI--------GDW 326
Db 232 LTVIGAFLNLVVLRFLVASADW 253

RESULT 3
T13807
potassium channel protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13807
R;Goldstein, S.A.; Price, L.A.; Rosenthal, D.N.; Pausch, M.H.
Proc. Natl. Acad. Sci. U.S.A. 93, 13256-13261, 1996
A;Title: ORK1, a potassium-selective leak channel with two pore domains cloned from Dros
A;Reference number: Z17770; MUID:97075152
A;Accession: T13807
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1001 <GOL>
A;Cross-references: EMBL:U55321; NID:g3808067; PID:g3808068; PIDN:AAC69250.1
C;Genetics:
A;Gene: ORK1
A;Cross-references: FlyBase:FBgn0017561
A;Map position: 1

Query Match 11.7%; Score 326; DB 2; Length 1001;
Best Local Similarity 22.9%; Pred. No. 1.2e-14;
Matches 123; Conservative 93; Mismatches 193; Indels 128; Gaps 20;

Qy 73 KWKTVVAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETL 132
Db 5 RW---ILLLIFYISYLMFGAAIYYHIEHGEEK-------ISRAEQRKAQIAINEYLLEEL 54

Qy 133 -----IQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPS 181
Db 55 GDKNTTTQDEILQRISDYCDKPVTLPPTYDDTPYTWTFYHAFFFAFTVCSTVGYGNISPT 114

Qy 182 TEGGKIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVS------QTK 235
Db 115 TFAGRMIMIAYSVIGIPVNGILFAGLGE----YFGRTFEAIYRRYKKYKMSTDMHYVPPQ 170

Qy 236 IRVISTILF-ILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVA--GGN 292
Db 171 LGLITTVVIALIPGIALFLLLPSWVFTYFENWPYSISLYYSYVTTTTIGFGDYVPTFGAN 230

Qy 293 AGINYREW---YKPLVWFWILVGLAYFAAVLSMIGDWLRVLSKK----TKEEVGEIKAHA 345
Db 231 QPKEFGGWFVVYQIFVIVWFIFSLGYLVMIMTFITRGLQ--SKKLAYLEQQLSSNLKATQ 288

Qy 346 AEWKANVTAEFRETRRRLS-------------VEIHDKLQRAATIRSMERRR-----LGL 387
Db 289 NRIWSGVTKDVGYLRRMLNELYILKVKPVYTDVDIAYTLPRSNSCPDLSMYRVEPAPIPS 348

Qy 388 DQRAHSL--DMLSPEKRS--VFAALDTGRFKASSQESINNRP-------------NNLRL 430
Db 349 RKRAFSVCADMVAAQREAGMVHANSDTELSKLDREKTFETAEAYRQTTDLLAKVVNALAT 408

Qy 431 KGP-----EQLNKHG--QGASEDNI---------INKFGSTSRLTKRKNKDLKKTLPE-- 472
Db 409 VKPPPAEQEDAALYGGYHGFSDSQILASEWSFSTVNEFTSPRRPRARACSDFNLEAPRWQ 468

Qy 473 ----------------DVQKIYKTFRN----------------YSLDEEKKEEETEK 497
Db 469 SERPLRSSHNEWTWSGDNQQIQEAFNQRYKGQQRANGAANSTMVHLEPDALEEQLKK 525

RESULT 4
T43509
probable potassium channel chain n2P38 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C;Accession: T43509
R;Wang, Z.W.; Salkoff, L.
submitted to the EMBL Data Library, August 1998
A;Description: Potassium channels in C. elegans.
A;Reference number: Z22450
A;Accession: T43509
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-329 <WAN>
A;Cross-references: EMBL:AF083652; PIDN:AAC32863.1

Query Match 11.3%; Score 315.5; DB 2; Length 329;
Best Local Similarity 31.6%; Pred. No. 1.5e-14;
Matches 86; Conservative 48; Mismatches 99; Indels 39; Gaps 9;

Qy 78 VAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETL----- 132
Db 9 LSLIVCTLTYLLVGAAVFDALETENEILQRKLVQRVR-EKLKTKYNMSNADYEILEATIV 67

Qy 133 --IQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCI 190
Db 68 KSVPH-----KAGY----------QWKFSGAFYFATTVITTIGYGHSTPMTDAGKVFCM 111

Qy 191 LYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFIL---- 246
Db 112 LYALAGIPLGLIMFQSIGERMNTFAAKLLRFIRRAAGKQPI-----VTSSDLIIFCTGW 165

Qy 247 AGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAG-INYREWYKPLV 305
Db 166 GGLLIFG--GAFMFSSYENWTYFDAVYYCFVTLTTIGFGDYVALQKRGSLQTQPEYVFFS 223

Qy 306 WFWILVGLAYFAAVLSMIGDWLRVLSKKTKEE 337
Db 224 LVFILFGLTVISAAMNLL--VLRFLTMNTEDE 253

```
RESULT   5
T32347
outward rectifier potassium channel homolog twk-23 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T32347
R;Murray, J.; Wohldmann, P.; O'Neal, D.
submitted to the EMBL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid F34D6.
A;Reference number: Z21153
A;Accession: T32347
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-336 <MUR>
A;Cross-references: EMBL:AF025454; PIDN:AAC71151.1; GSPDB:GN00020; CESP:F34D6.3
A;Experimental source: strain Bristol N2; clone F34D6
C;Genetics:
A;Gene: twk-23; CESP:F34D6.3
A;Map position: 2
A;Introns: 44/3; 102/1; 136/1; 180/1; 207/1; 265/2; 296/3


  Query Match             11.0%;  Score 307;  DB 2;  Length 336;
  Best Local Similarity   30.3%;  Pred. No. 6e-14;
  Matches   84;  Conservative   50;  Mismatches  101;  Indels   42;  Gaps    9;

Qy      78 VAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHAL 137
           ::: |  : ||: |  || |||   | |   :                |::|   ::  |
Db       9 LSLIVCTLTYLLVGAAVFDALETENEILQVRGLG------------EPRKLVQRVREKL 55

Qy     138 ----DADNAG--------VSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGG 185
               :  ||         |  : : :     |    ||:|| ||||||||||:  | |: |
Db      56 KTKYNMSNADYEILEATIVKSVPHKA--GYQWKFSGAFYFATTVITTIGYGHSTPMTDAG 113

Qy     186 KIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFI 245
           |:||:|||: ||||   :   ||::: |   | :  : :   |: :      | |: | |
Db     114 KVFCMLYALAGIPLGLIMFQSIGERMNTFAAKLLRFIRRAAGKQPI------VTSSDLII 167

Qy     246 L----AGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAG-INYREW 300
           | ::|    | :|   | ||  :::|:  |||||:||||:||    | :  :
Db     168 FCTGWGGLLIFG--GAFMFSSYENWTYFDAVYYCFVTLTTIGFGDYVALQKRGSLQTQPE 225

Qy     301 YKPLVWFWILVGLAYFAAVLSMIGDWLRVLSKKTKEE 337
           |      :|| ||   :| ::::   || |:  |::|
Db     226 YVFFSLVFILFGLTVISAAMNLL--VLRFLTMNTEDE 260


RESULT   6
T43361
probable potassium channel chain n2P20 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C;Accession: T43361
R;Wang, Z.W.; Salkoff, L.
submitted to the EMBL Data Library, August 1998
A;Description: Potassium channels in C. elegans.
A;Reference number: Z22450
A;Accession: T43361
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-364 <WAN>
A;Cross-references: EMBL:AF083646; PIDN:AAC32857.1


  Query Match             10.8%;  Score 300.5;  DB 2;  Length 364;
  Best Local Similarity   26.8%;  Pred. No. 1.9e-13;
  Matches  106;  Conservative   78;  Mismatches  124;  Indels   87;  Gaps   19;

Qy      75 KTVVAIFVVV--VVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHV----CVSPQE 128
           |:  |: :::    ||: | :||  ||     |:|:|   :: | : | :      | ::
Db       7 KSARALLLILSTFTYLLFGAMVFDKLE-----SEKDTWVRDEIERITDRLKHKYNFSERD 61

Qy     129 LETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIF 188
           |     |  :|    :  |   :     |    ||:||  ||||:|||: ||||  ||:|
Db      62 L-----HLFEA--IAIKSIPQQA--GYQWQFAGAFYFATVVITTVGYGHSAPSTNAGKLF 112

Qy     189 CILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRK------KQVSQTKIRVIS-T 241
           |:::|:||:|:   :   ||::: |    |: :      :      ::|: | : ::| |
Db     113 CMIFALFGVPMGLIMFQSIGERVNTFIAYSLHKFRDSLHQQGFTCLQEVTPTHLLMVSLT 172

Qy     242 ILF--ILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYRE 299
           | |  |::|  :| |        || |:  :: || ::| :|:|||| |      :|  :
Db     173 IGFMVIVSGTYMFHT--------IEKWSIFDAYYFCMITFSTIGFGDLVP--LQQVNALQ 222

Qy     300 WYKPLVWF----WILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAE 355
             :||  |    :||:||| |:| ::::             :| : ::| |    |||
Db     223 -DQPLYVFATIMFILIGLAVFSACVNLL------------VLGFMASNADE----VTAA 264

Qy     356 FRE----------TRRRLSVEIHDKLQRAATIRSMERRRLGLDQRAHSLDMLS------- 398
           ||           ||  |       :|: :|:  :     |  :| :|:   |
Db     265 QREPPSAIVLERFTRNSLVDSQIFNIQKHSTVGVLP----GRPRRMYSIVPNSTADVHLR 320

Qy     399 --PEKRSVFAALDTGRFKASSQE---SINNRPNNL 428
             :||:   :  | ||        |:  || |:
Db     321 RRSTRRSIQDTVCCGCFKPRPPRHRFSLTRRPTNI 355


RESULT   7
T25392
hypothetical protein T28A8.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T25392
R;Lloyd, C.
submitted to the EMBL Data Library, March 1997
A;Reference number: Z20027
A;Accession: T25392
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-393 <WIL>
A;Cross-references: EMBL:Z92813; PIDN:CAB07286.1; GSPDB:GN00021; CESP:T28A8.1
A;Experimental source: clone T28A8
C;Genetics:
A;Gene: CESP:T28A8.1
A;Map position: 3
A;Introns: 73/1; 112/3; 179/2; 209/3; 287/2; 310/3; 364/2


  Query Match             10.7%;  Score 298.5;  DB 2;  Length 393;
  Best Local Similarity   27.1%;  Pred. No. 2.9e-13;
  Matches   85;  Conservative   50;  Mismatches   94;  Indels   85;  Gaps   11;

Qy      74 WKTV-------VAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSP 126
           |||        |:: |: |||:  |  :|  ||||      | : :      | ::
Db       4 WKTYARIILAHVSLIVLSVVYVGFGAFLFYQLEQP------NEVEVRARNIERFNI---- 53

Qy     127 QELETLIQHALDADNAGVSP-------------------------IG------NSSNNS 154
             :|:|  :   :|:                            ||       :
Db      54 -HKRQMIEHLWEMRESGIGQHVVEDLAVKYVDNVTRILFEAFDTHCIGAKHLRPGGEDED 112

Qy     155 SHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLFGFLLAGIGDQLGTI 214
           :|   :| ||  |::|||||||: | |  ||: |||||:||:||   :|  : | :|
Db     113 YNWTYMTALFFTTTLLTTIGYGNLTPVTGRGKLLCILYALFGVPL---ILITVAD-IGKF 168

Qy     215 FGKSIARVEKVFRK--KQVSQTKIRVIST---------------------ILFILAGCI 250
           ::| ::   :||  :: |: |  |||:                        |  |:|  :
Db     169 LSENIVQLYTWYRKLREKCSKQKYSVISSKDDKNKEGDLNLDHLENYISIPIFLIVAILL 228

Qy     251 VFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWIL 310
           ::|  ||:    |||       ||  :|:|||||| |          ||:|  |   :|:
Db     229 SYITFGAVVLSMWEGWDFFSGFYFSFITMTTVGFGDIVP------LKREYY-ILDLCYII 281

Qy     311 VGLAYFAAVLSMIG 324
           :||:     : ::|
Db     282 IGLSITTMCIDLVG 295
```

```
RESULT   8
H88124
protein T12C9.3 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C;Accession: H88124
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: H88124
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1910 <STO>
A;Cross-references: GB:chr_II; PIDN:AC71141.1; PID:g1086770; GSPDB:GN00020; CESP:T12C9.3
A;Note: proline-rich
C;Genetics:
A;Gene: T12C9.3
A;Map position: 2


  Query Match             10.5%;  Score 294.5;  DB 2;  Length 1910;
  Best Local Similarity   21.1%;  Pred. No. 4.6e-12;
  Matches  119;  Conservative   90;  Mismatches  193;  Indels  163;  Gaps   22;

Qy      21 PAAAPVCQPKSATNGQPPAP-APTP---TPRLSISSRATVVARMEGTSQGGLQTVMKWKT 76
           ||    |  |       || |  |||   : | ||        || :   :   || : |:
Db     140 PATRKACLSKQV---HPPIPHHPTPPQFSRRFSIFPGLLESARPDDETTTTLQNIRKYAK 196

Qy      77 V----VAIFVVVVVYLVTGGLVFRALEQPFESSQK----NTIALEKA------------- 115
           :    : : | | :|   |  :|  || | |    |     |||  ::
Db     197 LALPHIVLVVCVCIYATIGAWIFYTLESPNEDRLKETGRKTIAEMRSNLIYKINNNEKEV 256

Qy     116 --EFLRDHVCVSPQEL-----ETLIQHA-------------LDADNAGVSPIGNSSNNSS 155
             | :   : :  ::|     |  ::::              :||  |    |:|
Db     257 WKEDIEKELMLYSEKLYKAFKEQYVRYSDVRTIGFEGRSSYEEADETG----GDSERKRR 312

Qy     156 H--------------WDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLFG 201
           |              |   || ||| | : |||||| | |   |:: |:|:|:|:|| |:
Db     313 HRHGNKRGDRGSEKMWTTSSALFFAATTMATIGYGNIVPVTPLGRLACVLFALFGAPIAI 372

Qy     202 FLLAGIGDQLG--TIF-----GKSIARVEKVFRK------------------------- 228
             :  :|  |   ||:      |  ||::  :::
Db     373 ITIGDLGKFLSECTIWLYKHMRKGSARLDSAWKRFRGLEDSISDDLESASKNQDSSILDM 432

Qy     229 --KQVSQTKIRVISTILFILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGD 286
           ::  :::: |:     ||    :::    ::|  :| |: ::: |:  ::|||:||||
Db     433 DMDEIDKSEVPVLMVFTIIL----LYIAFGGILFSILEDWSYMDAFYYSFISLTTIGFGD 488

Qy     287 FVAGGNAGINYREWYKPLVWFWILVGLAYFAAVLSMIG----------------DWLRV 329
           |   :        |  ::  :: |||:     : : |                 | |:
Db     489 IVPENHD-------YIAIMLIYLGVGLSVTTMCIDLAGIQYIQKIHYFGRKFQGTDLLQY 541

Qy     330 LSKKTK----------EEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRS 379
           | ||            ||:     || |       :|   : :|  :: ::    :   :
Db     542 LKKKRMLERRLAMGQGEEILRKYVHAVE-------KFEREQEQLQQKMEEEDPPSIESKG 594

Qy     380 MERRRLGLDQRAHSL-----------DMLSPEKRSV--FAALDTGRFKASSQESI---NN 423
             :  : :|   :              |: ||  ||  |         | ||       |
Db     595 FDNSMMRIDDSLSAFQLRFYDTYDEEDLFSPTIHSVRSFQPSVWSHSSARSQSFCRFQRN 654

Qy     424 RPNNLRLKGPEQLNKHGQGASEDNI 448
           |  :    ||  |::|   ::| ::
Db     655 RGASWDESGP-SLSEHCSLSTEPSV 678


RESULT   9
T19860
hypothetical protein C40C9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T19860
R;Hembry, C.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19188
A;Accession: T19860
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-334 <WIL>
A;Cross-references: EMBL:Z70266; PIDN:CAA94204.1; GSPDB:GN00028; CESP:C40C9.1
A;Experimental source: clone C40C9
C;Genetics:
A;Gene: CESP:C40C9.1
A;Map position: X
A;Introns: 34/1; 60/2; 98/1; 145/3; 160/3; 181/1; 204/1; 252/2; 279/2; 306/3


  Query Match             10.4%;  Score 290.5;  DB 2;  Length 334;
  Best Local Similarity   28.6%;  Pred. No. 8.4e-13;
  Matches   89;  Conservative   67;  Mismatches   94;  Indels   61;  Gaps   15;

Qy      75 KTVVAIFVVV--VVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHV----CVSPQE 128
             |:  |: :::    ||: | :||  ||     |:|:|   :: | : | :      | ::
Db       7 KSARALLLILSTFTYLLFGAMVFDKLE-----SEKDTWVRDEIERITDRLKHKYNFSERD 61

Qy     129 LETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIF 188
           |     |  :|    :  |   :     |    ||:|| ||||:|||: |||| ||:|
Db      62 L-----HLFEA--IAIKSIPQQA--GYQWQFAGAFYFATVVITTVGYGHSAPSTNAGKLF 112

Qy     189 CILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRK------KQVSQTKIRVIS-T 241
           |:::|:||:|:    :   ||::: |    |: :       :       ::|: | : ::| |
Db     113 CMIFALFGVPMGLIMFQSIGERVNTFIAYSLHKFRDSLHQQGFTCLQEVTPTHLLMVSLT 172

Qy     242 ILF--ILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYRE 299
           | |  |::|  :| |        || |:  :: || ::| :|:|||| |      :|  :
Db     173 IGFMVIVSGTYMFHT--------IEKWSIFDAYYFCMITFSTIGFGDLVP--LQQVNALQ 222

Qy     300 WYKPLVWF----WILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAE 355
             :||  |    :||:||| |:| ::::              :| : ::| |    |||
Db     223 -DQPLYVFATIMFILIGLAVFSACVNLL------------VLGFMASNADE----VTAA 264

Qy     356 FRETRRRLSVE 366
           ||    : :|
Db     265 QREPPSAIVLE 275


RESULT  10
T45032
hypothetical protein Y39B6B.f [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45032
R;Wilson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.; Burto
raser, A.; Fulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, M.; Jo
 B.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifken, L.; Roopra, A.; Saunders, D.
Nature 368, 32-38, 1994
A;Authors: Shownkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonnhammer, E.
tock, L.; Wilkinson-Sproat, J.; Wohldman, P.
A;Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.
A;Reference number: S43531; MUID:94150718
A;Accession: T45032
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-392 <WIL>
A;Cross-references: EMBL:AL132896; NID:g6434440; PIDN:CAB60911.1; PID:g6434446
A;Experimental source: clone Y39B6B
C;Genetics:
A;Map position: 3
A;Introns: 47/2; 82/2; 106/3; 151/1; 220/1; 260/3; 370/3
A;Note: Y39B6B.f


  Query Match             10.1%;  Score 282.5;  DB 2;  Length 392;
```

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  Best Local Similarity   31.7%;  Pred. No. 3.8e-12;
  Matches   77;  Conservative   46;  Mismatches   97;  Indels   23;  Gaps    8;

Qy      95 FRALEQPFESSQKNTIALEKAEFLRDHVC---VSPQELETLIQHALDADNAGVSPIGNSS 151
           |  :| | |  ::    |:     || :    :   |:: |    |:   | :: |
Db     118 FSRIEYPLEKIEREAY-LDYQNQWRDRLIQLDIDESEIDKLF---LNIREAALNGIWMDR 173

Qy     152 NNSS--HWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLFGFLLAGIGD 209
           | :|  :|  | |||||||:|:|:||| ::| || ||:| ||| : ||||   ||: |
Db     174 NLTSDPNWTFGQAFFFAGTLISTVGYGRVSPRTEYGKLFTILYCVIGIPLTLALLSAIVA 233

Qy     210 QL----GTIFGKSIARVEKVFRKKQVSQTKIRVI--STILFILAGCIVFVTIPAVIFKYI 263
           ::      : |    |:  :|    :    : |:  | :||: |       ||| :|  |
Db     234 RMREPSHKLRGLLNQRLGHLFTVNHIQLIHVGVVFASLLLFVFA-------IPAWVFSSI 286

Qy     264 E-GWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVLSM 322
           |  |: |:: |:  |:|||:| |||  | :   ::|  ||     ::: ||      |:
Db     287 ETDWSYLDAFYYCFVSLTTIGLGDFEPGDDPNQSFRGLYKIGATVYLMGGLCCMMLFLAT 346

Qy     323 IGD 325
           : |
Db     347 LYD 349


RESULT  11
T24265
hypothetical protein T01B4.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T24265
R;Wilkinson, J.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19866
A;Accession: T24265
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-522 <WIL>
A;Cross-references: EMBL:Z70036; PIDN:CAA93875.1; GSPDB:GN00028; CESP:T01B4.1
A;Experimental source: clone T01B4
C;Genetics:
A;Gene: CESP:T01B4.1
A;Map position: X
A;Introns: 95/3; 142/1; 224/3; 290/1; 458/1


  Query Match             9.6%;  Score 268.5;  DB 2;  Length 522;
  Best Local Similarity   22.3%;  Pred. No. 5.2e-11;
  Matches  120;  Conservative   89;  Mismatches  181;  Indels  147;  Gaps   21;

Qy      78 VAIFVVVVVVYLVTGGLVFRALE---QPFE--------SSQKNTIALEKAEFLRDHVCVSP 126
           : : :::: |   || :|:|||   |  |          |: : :|:   | |:   |
Db      39 IMLILIIILGYACLGGYMFQALEYDQQQLELEAEKRVRLSESSLLAVNLLEHLKQMNCGQS 98

Qy     127 QE-------LETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIA 179
           |        :| || : :    |              ||  :: ||: |: |||||||:|
Db      99 NEKRCLELITKTFIQRSDEERGEG-----------WRWDFWNSVFFSATIFTTIGYGNLA 147

Qy     180 PSTEGGKIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSI-----ARVEKVFRKKQVSQT 234
           |  |:|  |:| : ||||  |:|   | :|   : | |       ::| | :||   :
Db     148 CKTNLGRIATIIYGMIGIPLMLFVLKNFG-ELCVKWAKKIQFNVQQCLKKCFGRKQKRAS 206

Qy     235 KIRVIST--------------------ILFILAGCIVFVTIPAVIFKYIEGWTALESIY 273
           :  |::                     : : |   ::|| : : :  : | |  | : |
Db     207 SLASITSKEMLEVFFEVPEDDKEDTTFQLRWGLLVIVLFVVLCSFVVSFWENWDFLTAFY 266

Qy     274 FVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWIL--VGLAYFAAVLSMIGD------ 325
           |  |:|:|:|||| |          :  :     ::|  :||| || | ::: :
Db     267 FFFVSLSTIGFGDIVP---------DHPRTACALFVLYFIGLALFAMVYAILQERVENQY 317

Qy     326 -W-LRVLSKKTKEEVGEIKAHAAEWKA---NVTAEFRETRRRLSVEIHDKLQRAATIRSM 380
            | | :: :| :|:: :      | ||   ::    :|  |   : : | | |   ::
Db     318 MWALELIDQKYQEKLKQDMYDEDEKKADKNDMHFSKKEPVRGPRILLQD-LLRGPDLKIS 376

Qy     381 ERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGP-EQLNKH 439
             ||   |  | |:   : ::       || ||          |        | |: : |
Db     377 GGRRSSSD--ASSVITEASDE-------DTRHFKV-------GRAILAEAFAPDERASNH 420

Qy     440 GQGASEDNIINKFGSTSRLTKRKNKDLKKTLPEDVQKIYKTFR---------NYSLDEEK 490
           |   :   : |:  |                 :: |  :|          ||| ||
Db     421 GTQLNSCTVSNEHDSC----------------QIEAIVFSFHFISFINFQFNYSSDESL 463

Qy     491 KEEETEKMCNS-----------------DNSSTAM-------LTDCIQQHAELENG 522
           :| : |    |                  | : |::       |   :::  | |||
Db     464 EEHQLETYDTSGTPPPYGDPTPTTNFQTRDETVTSLAEKTPLSLNKVLEEENEDENG 520


RESULT  12
T21834
hypothetical protein F36A2.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T21834
R;Lennard, N.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19476
A;Accession: T21834
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-528 <WIL>
A;Cross-references: EMBL:Z81077; PIDN:CAB03071.1; GSPDB:GN00019; CESP:F36A2.4
A;Experimental source: clone F36A2
C;Genetics:
A;Gene: CESP:F36A2.4
A;Map position: 1
A;Introns: 45/3; 81/3; 114/3; 151/3; 195/1; 306/1; 326/1; 368/2; 413/1; 464/2; 494/1


  Query Match             9.5%;  Score 265.5;  DB 2;  Length 528;
  Best Local Similarity   22.2%;  Pred. No. 8.6e-11;
  Matches  122;  Conservative   86;  Mismatches  163;  Indels  179;  Gaps   26;

Qy      84 VVVYLVTGGLVFRALE----------------------QPFE------SSQKNTIALEKA 115
           |:|:|:: | :||: ||                      : ||      |   |    :|:
Db      25 VVLYIILGAIVFQMLEGEHLDNFSDFNPKKHFGPKMVDKFFETIFRRWSKGAN---FKKS 81

Qy     116 EFLRDHVCVSPQ--------------------ELETLI----QHALDADNAGVSPI--- 147
              :||:    |                    :| ||     :  :|  |  |  :
Db      82 ALKKDHMAKIEQNAKDYVDKLWSVAKRDRDKYKNVEDLIKSVKEDTVDDFNDYVDTVFYA 141

Qy     148 -----GNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLFGF 202
                  :|  ||  :: ||  |::|:|||| :|||| ||::| ::| : ||||
Db     142 HRAVRHGYDEDSPTWDFANSVFFTTTMLTSIGYGYVAPSTFGGRLFGVIYCLIGIPLTLV 201

Qy     203 LLAGIGDQLG-TIF-------GKSIARVEKVFRKKQVSQ-----------------TKIR 237
           :| :   |  |||       | :    |  || :|                    ::|
Db     202 TVANVAKFLSETIFFLHYELWNKCLEWKRK--RKGEVEADPLQPMFGDDENEEEILDRVR 259

Qy     238 VIS----TILFILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDF-VAGGN 292
           ::     |: | :    |:  | | : :| | || :||:||: ::: ||||||   : ||
Db     260 LVRFPPLTVFFFV---FVYGCIAAWVVRYWETWTYVESLYFIFISILTVGFGDIRPSPGN 316

Qy     293 AGINYREWYKPLVWF---WILVGLAYFAAVLSMIGDW----LRVLSKKTKEE-----VGE 340
                   :|    :::||:       : ::|      :  | :| |       : |
Db     317 -----------IWVTLAFVVVGVILTTMCMDVVGRMYLKEIHYLGRKLKSSNPFYLLRE 364

Qy     341 IKAHAAEWKANVTAEFRETRRRLSV--------------EIHDKLQRAATIRSMERRRL 385
           ||                 ||| ::               : :::| |  : |  |:||
Db     365 AKAR--------------RRRAAMASLLAQLAKGMIFAHKDYNELARKKSKRKKEKRR- 408

Qy     386 GLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGPEQLNKHGQGASE 445
                :| |    | :: :|| |        |  : ::    ::||                |
Db     409 ----GSHVL----PNEKFMFARLPPD--PPSDCQVVSTSAYSVRLAWAPPF-------SP 451

Qy     446 D-----NIINKFGSTSRLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEEETEKMC- 499
           |     ||  :  :|:      :    | : |     ||   |  : :   |  :  :|
Db     452 DPDLTYNIRYRLNATAVFKDGQRSPLSRALFIKTDKI--EFHKHCVGHSKTIDVMDSICE 509
```

```
Qy    500 NSDNSSTAML 509
            || :|:|
Db    510 KEDNETTALL 519
```

RESULT 13
T26229
hypothetical protein W06D12.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T26229
R;Basham, V.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z20177
A;Accession: T26229
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-444 <WIL>
A;Cross-references: EMBL:Z82073; PIDN:CAB04923.1; GSPDB:GN00023; CESP:W06D12.2
A;Experimental source: clone W06D12
C;Genetics:
A;Gene: CESP:W06D12.2
A;Map position: 5
A;Introns: 70/3; 127/1; 170/1; 197/3; 326/1; 405/3

  Query Match 9.5%; Score 264.5; DB 2; Length 444;
  Best Local Similarity 20.3%; Pred. No. 8e-11;
  Matches 103; Conservative 80; Mismatches 170; Indels 155; Gaps 16;

```
Qy     83 VVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCV----------------S 125
          |::||   |  :|   |   | | |:    :    ||  :                  |
Db     23 VLIVYSFLGAGLFVLCEAENEKSLKHE---DNMRVLRTSIAAKQVFVQRLQNMYSGNGSS 79

Qy    126 PQELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGG 185
          :  || ::  |   :| :  |   |  : ||:    ::|||: ||||||::|  |  |
Db     80 SEFSETKLRRVLSEYDAAMG-ISIDSKMKTRWDIWGGLYYAGTIYTTIGYGDLAAETIWG 138

Qy    186 KIFCILYAIFGIPLFGFLLAGIGDQLGTI---FGKSIARV------EKVFRKK------- 229
          :|  :|||: |||:   :|   |: |      | ::| |       :|: |:|
Db    139 RICTMLYAMIGIPIVINILNDWGNMLFYFVDHFWQNIGRQWIQSLRQKLRRRKVQSLEEG 198

Qy    230 --------QVSQTK-------------IRVISTILFILAGCIVFVTIPAVIFKYIEGWT 267
                 : | |                : |:  : | :  |: :       | | | ||
Db    199 SIDKTPLMETSSTPPSPQNPNGTRPIPLLLVLIVLFFWMIQCVAY-------FAYFENWT 251

Qy    268 ALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVLSMIGDWL 327
          ||:|| :::||:|||||      :                |: :   ||::   :
Db    252 LFESVYFFFISMTTIGFGDFTPSHTVAVG-------------GIVFILGGLSVVSMCI 296

Qy    328 RVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSMERRRLGL 387
          |:              :  :   | :  :|:  :  : |  ||      :: :|:
Db    297 NVI-----------------QMQLEFIFNQIVQRIENDFKNTLSVAA--EESRKKSIGV 336

Qy    388 DQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGPEQLNKHGQGASEDN 447
                    | | ::|  : |             :|  |               |
Db    337 --------------SEFGSIDPSKKK-----------TMRTDG-------------N 355

Qy    448 IINKFGSTSRLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEEETEKMCNSDNSSTA 507
          :  |:     :    || | : :    :|:*           :| :|  || ||   :|:
Db    356 VAEKYSENMEM---GNKLLMRFMSNHQKKML----------NEKFDERAKMRNSGTQTTS 402

Qy    508 MLTDCIQQHAELENGMIPTDTKDREPEN 535
          :     | ||        | :: :|::
Db    403 QIKVASVQTAERYEQTWDEDPEEEQPKS 430
```

RESULT 14
T16426
hypothetical protein F52E4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
C;Accession: T16426
R;Martin, J.
submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid F52E4.
A;Reference number: Z18512
A;Accession: T16426
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-551 <MAR>
A;Cross-references: EMBL:U56964; NID:g1293826; PID:g2078439; PIDN:AAB54033.1; GSPDB:G
A;Experimental source: strain Bristol N2; clone F52E4
C;Genetics:
A;Gene: CESP:F52E4.4
A;Map position: X
A;Introns: 14/3; 65/3; 95/2; 118/1; 165/3; 267/1; 297/2; 334/3; 385/2; 477/1; 513/2

  Query Match 9.4%; Score 264; DB 2; Length 551;
  Best Local Similarity 20.3%; Pred. No. 1.2e-10;
  Matches 108; Conservative 94; Mismatches 205; Indels 124; Gaps 16;

```
Qy     79 AIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETL------ 132
          :: ::|::|   || :|  :|    :  |      : | :    ||| | | ::
Db     24 SLLMLVLLYSFLGGFIFDRIETNAHAEMK------RNERINRTACVS-QILHSIHRWSHN 76

Qy    133 ----IQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIF 188
              :|:| |  :          :  | |:  :|  :   ::||:|| ||| |  |::|
Db     77 QTHKVQYAEDIADC----FEPEKDERSEWNFVTATLYGFGIVTTLGYNRIAPITYTGRMF 132

Qy    189 CILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKI--------RVIS 240
          ||:| | |||:   ::| :|  |    | |  ::|   :::::|:  :         :
Db    133 CIVYGICGIPVTMIIIANVGQYLNNFAGDSRRKIEAYRQQRRMSKASLAGKIYKESSIQV 192

Qy    241 TILFILAGCIVFVTIPAVIFKYIEG-WTALESIYFVVVTLTTVGFGDFVAGGNAGINYRE 299
          | | :|   :::| : |::   : |       :||  : || : ||  |         |
Db    193 TSLALLCVFLIYVAVGALLLPLLNGELDFFNGLYFNFLCLTAIDFGQLVP-------IRV 245

Qy    300 WYKPLVWFWILVGLA------------------------------YFAAVLSMIGDWLR 328
             |: : :: :|||                              :|      : | |
Db    246 ELLPITFLYVCIGLAITTIAINIGSEYMKKLHYWGKKMKNAAQTRIWFGGKTLKVRDLLH 305

Qy    329 VLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM-------- 380
          : ||   | | | |    |      |   :| |     :::|:  |  : ||:
Db    306 AVGKKCGVEPGMIDALDLENVVERTIAMQEGREP-PEDLNDEPPREPSPRSIIHSPCSTR 364

Qy    381 ----------------------ERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASS 417
                               | |   |: ||:    |: :| ||       |:
Db    365 PSNPPMSPPSPREDHPFIFKMDAPAPRSPLPLPAYELDI----KKPIFQALSNEFMNQSA 420

Qy    418 QESINNRPNNLRLK-GPEQLNKH---------GQGASEDNII------NKFGSTSRLTKR 461
          || : |  :  :::   | :  |             ||  |       :    :: ||
Db    421 QEKLFNDLDTFQIEINTELVEDHKCESVIIIEPPATFEDMTIQHSLCVEDYEREEKVPKR 480

Qy    462 KNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEEETEKMCNSDNSSTAMLTDC 512
          :: |:    | :|:|:|   |  : :: |  :::       |   |::|
Db    481 -FREKKEMYGRDPRKLYET---YQEEWDRLERLSDRKHGPRRKSVLNLSNC 527
```

RESULT 15
T43357
potassium channel chain n2P16 homolog - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 11-Jan-2000
C;Accession: T43357
R;Wang, Z.W.; Kunkel, M.T.; Wei, A.; Butler, A.; Salkoff, L.
Ann. N. Y. Acad. Sci. 868, 286-303, 1999
A;Title: Genomic organization of nematode 4TM K+ channels.
A;Reference number: Z22446; MUID:99342707
A;Accession: T43357
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-555 <WAN>
A;Cross-references: EMBL:AF083645; PIDN:AAC32856.1

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  Query Match             9.4%;  Score 264;  DB 2;  Length 555;
  Best Local Similarity   20.3%;  Pred. No. 1.2e-10;
  Matches  108;  Conservative   94;  Mismatches  205;  Indels  124;  Gaps   16;

Qy      79 AIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETL------ 132
           :: ::|::|   || :|  :|    :  |      : | :    ||| | | ::
Db      28 SLLMLVLLYSFLGGFIFDRIETNAHAEMK------RNERINRTACVS-QILHSIHRWSHN 80

Qy     133 ----IQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIF 188
               :|:| |  :          :  | |:  :|  :   ::||:||  ||| |  |::|
Db      81 QTHKVQYAEDIADC----FEPEKDERSEWNFVTATLYGFGIVTTLGYNRIAPITYTGRMF 136

Qy     189 CILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKI--------RVIS 240
           ||:| | |||:   ::| :|  |    | |  ::|   :::::|:  :         :
Db     137 CIVYGICGIPVTMIIIANVGQYLNNFAGDSRRKIEAYRQQRRMSKASLAGKIYKESSIQV 196

Qy     241 TILFILAGCIVFVTIPAVIFKYIEG-WTALESIYFVVVTLTTVGFGDFVAGGNAGINYRE 299
           | | :|   :::| : |::   : |       :||  : || : ||  |         |
Db     197 TSLALLCVFLIYVAVGALLLPLLNGELDFFNGLYFNFLCLTAIDFGQLVP-------IRV 249

Qy     300 WYKPLVWFWILVGLA------------------------------YFAAVLSMIGDWLR 328
              |: : :: :|||                             :|      : | |
Db     250 ELLPITFLYVCIGLAITTIAINIGSEYMKKLHYWGKKMKNAAQTRIWFGGKTLKVRDLLH 309

Qy     329 VLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM-------- 380
            : ||   | | | |   |     |   :| |     :::|:  |  : ||:
Db     310 AVGKKCGVEPGMIDALDLENVVERTIAMQEGREP-PEDLNDEPPREPSPRSIIHSPCSTR 368

Qy     381 ----------------------ERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASS 417
                                   |  |   |: ||:    |: :| ||       |:
Db     369 PSNPPMSPPSPREDHPFIFKMDAPAPRSPLPLPAYELDI----KKPIFQALSNEFMNQSA 424

Qy     418 QESINNRPNNLRLK-GPEQLNKH---------GQGASEDNII------NKFGSTSRLTKR 461
           || : |  :  :::   | :  |              ||  |        :    :: ||
Db     425 QEKLFNDLDTFQIEINTELVEDHKCESVIIIEPPATFEDMTIQHSLCVEDYEREEKVPKR 484

Qy     462 KNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEEETEKMCNSDNSSTAMLTDC 512
             :: |:    | :|:|:|   |  : :: |  :::       |  .|::|
Db     485 -FREKKEMYGRDPRKLYET---YQEEWDRLERLSDRKHGPRRKSVLNLSNC 531


Search completed: September 21, 2002, 09:50:06
Job time: 4297 sec
```

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GenCore version 4.5

OM protein - protein search, using sw model

Run on: September 21, 2002, 09:49:14 ; Search time 37.61 Seconds
(without alignments)
559.019 Million cell updates/sec

Title: US-09-729-920-2
Perfect score: 2795
Sequence: 1 MKFPIETPRKQVNWDPKVAV.....IPTDTKDREPENNSLLEDRN 543

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2697	96.5	538	1	CIWA_HUMAN	P57789 homo sapien
2	2658.5	95.1	538	1	CIWA_RAT	Q9jis4 rattus norv
3	1251.5	44.8	411	1	CIW2_MOUSE	P97438 mus musculu
4	1218.5	43.6	426	1	CIW2_HUMAN	O95069 homo sapien
5	812.5	29.1	393	1	CIW4_HUMAN	Q9nyg8 homo sapien
6	790	28.3	398	1	CIW4_MOUSE	O88454 mus musculu
7	483	17.3	499	1	CIW5_HUMAN	O95279 homo sapien
8	403	14.4	336	1	CIW1_HUMAN	O00180 homo sapien
9	390.5	14.0	336	1	CIW1_MOUSE	O08581 mus musculu
10	352.5	12.6	409	1	CIW3_MOUSE	O35111 mus musculu
11	352.5	12.6	411	1	CIW3_RAT	O54912 rattus norv
12	350.5	12.5	365	1	CIW9_CAVPO	Q9j158 cavia porce
13	349.5	12.5	394	1	CIW3_HUMAN	O14649 homo sapien
14	334	11.9	374	1	CIW9_HUMAN	Q9npc2 homo sapien
15	333.5	11.9	313	1	CIW6_HUMAN	Q9y257 homo sapien
16	326	11.7	1001	1	ORK1_DROME	Q94526 drosophila
17	308	11.0	307	1	CIW8_MOUSE	Q9z2t1 mus musculu
18	300.5	10.8	307	1	CIW7_HUMAN	Q9y2u2 homo sapien
19	218	7.8	335	1	TWK8_CAEEL	P34410 caenorhabdi
20	217.5	7.8	691	1	TOK1_YEAST	P40310 saccharomyc
21	136	4.9	228	1	YWS1_CAEEL	Q10937 caenorhabdi
22	123	4.4	457	1	XYLT_LACBR	O52733 lactobacill
23	121.5	4.3	676	1	CIQ1_HUMAN	P51787 homo sapien
24	121.5	4.3	899	1	YA8D_SCHPO	Q09778 schizosacch
25	119	4.3	602	1	CIK5_RAT	P19024 rattus norv
26	115	4.1	602	1	CIK5_MOUSE	Q61762 mus musculu
27	115	4.1	897	1	CIQ5_HUMAN	Q9nr82 homo sapien
28	114.5	4.1	417	1	Y443_CHLPN	Q9z8a0 chlamydia p
29	114	4.1	1276	1	MDR2_CRIGR	P21449 cricetulus
30	114	4.1	2424	1	CCAA_RABIT	P27884 oryctolagus
31	113.5	4.1	1036	1	SMO_DROME	P91682 drosophila
32	113.5	4.1	1969	1	MYSA_CAEEL	P12844 caenorhabdi
33	113	4.0	723	1	ICAL_SHEEP	Q95208 ovis aries
34	112.5	4.0	528	1	YEP0_YEAST	P40039 saccharomyc
35	112.5	4.0	724	1	ATI1_VACCV	P24759 vaccinia vi
36	112	4.0	669	1	CIQ1_RAT	Q9z0n7 rattus norv
37	112	4.0	806	1	CIKB_HUMAN	Q92953 homo sapien
38	112	4.0	1077	1	HLES_DROME	Q02308 drosophila
39	112	4.0	2272	1	CCAE_MOUSE	Q61290 mus musculu
40	111.5	4.0	1433	1	REST_CHICK	O42184 gallus gall
41	111	4.0	2312	1	CCAE_HUMAN	Q15878 homo sapien
42	110	3.9	574	1	KCN2_MOUSE	P58390 mus musculu
43	110	3.9	726	1	ATI_CAMPC	Q05482 camelpox vi
44	110	3.9	813	1	NAH2_RAT	P48763 rattus norv
45	110	3.9	2505	1	CCAA_HUMAN	O00555 homo sapien

ALIGNMENTS

RESULT 1
CIWA_HUMAN
ID CIWA_HUMAN STANDARD; PRT; 538 AA.
AC P57789; Q9HB59;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Potassium channel subfamily K member 10 (Outward rectifying potassium
DE channel protein TREK-2) (TREK-2 K+ channel subunit).
GN KCNK10 OR TREK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20435789; PubMed=10880510;
RA Lesage F., Terrenoire C., Romey G., Lazdunski M.;
RT "Human TREK2, a 2P domain mechano-sensitive K+ channel with multiple
RT regulations by polyunsaturated fatty acids, lysophospholipids and Gs,
RT Gi, and Gq protein-coupled receptors.";
RL J. Biol. Chem. 275:28398-28405(2000).
CC -!- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL. PRODUCES RAPIDLY
CC ACTIVATING AND NON-INACTIVATING OUTWARD RECTIFIER K(+) CURRENTS.
CC ACTIVATED BY ARACHIDONIC ACID AND OTHER NATURALLY OCCURRING
CC UNSATURATED FREE FATTY ACIDS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN PANCREAS AND KIDNEY
CC AND TO A LOWER LEVEL IN BRAIN, TESTIS, COLON, AND SMALL INTESTINE.
CC -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC CHANNELS.
CC ----------

CC ----------
DR EMBL; AF279890; AAG15191.1; -.
DR MIM; 605873; -.
DR InterPro; IPR003280; 2poreK_channel.
DR InterPro; IPR000636; Cation_chan_non_lig.
DR InterPro; IPR001622; Channel_pore_K.
DR Pfam; PF00520; ion_trans; 1.
DR PRINTS; PR01333; 2POREKCHANEL.
KW Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW Glycoprotein.
FT DOMAIN 1 71 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 72 92 POTENTIAL.
FT DOMAIN 154 180 PORE-FORMING 1 (POTENTIAL).
FT TRANSMEM 182 202 POTENTIAL.
FT DOMAIN 203 233 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 234 254 POTENTIAL.
FT DOMAIN 263 294 PORE-FORMING 2 (POTENTIAL).

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FT   TRANSMEM     299    319       POTENTIAL.
FT   DOMAIN       320    538       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     144    144       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     147    147       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     148    148       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   538 AA;  59764 MW;  8EA615B08D147FBC CRC64;
```

```
  Query Match             96.5%;  Score 2697;  DB 1;  Length 538;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-161;
  Matches  526;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      18 VAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKTV 77
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13 VAVPAAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKTV 72

Qy      78 VAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHAL 137
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73 VAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHAL 132

Qy     138 DADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGI 197
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     133 DADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGI 192

Qy     198 PLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPA 257
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     193 PLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPA 252

Qy     258 VIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFA 317
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     253 VIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFA 312

Qy     318 AVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATI 377
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     313 AVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATI 372

Qy     378 RSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGPEQLN 437
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     373 RSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLKGPEQLN 432

Qy     438 KHGQGASEDNIINKFGSTSRLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEEETEK 497
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     433 KHGQGASEDNIINKFGSTSRLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKKEEETEK 492

Qy     498 MCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN 543
           |||||||||||||||||||||||||||||||||||||||||||||||
Db     493 MCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLLEDRN 538
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RESULT   2
CIWA_RAT
ID   CIWA_RAT       STANDARD;      PRT;   538 AA.
AC   Q9JIS4;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Potassium channel subfamily K member 10 (Outward rectifying potassium
DE   channel protein TREK-2) (TREK-2 K+ channel subunit).
GN   KCNK10 OR TREK2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20298807; PubMed=10747911;
RA   Bang H., Kim Y., Kim D.;
RT   "TREK-2, a new member of the mechanosensitive tandem-pore K+ channel
RT   family.";
RL   J. Biol. Chem. 275:17412-17419(2000).
CC   -!- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL. PRODUCES RAPIDLY
CC       ACTIVATING AND NON-INACTIVATING OUTWARD RECTIFIER K(+) CURRENTS.
CC       ACTIVATED BY ARACHIDONIC ACID AND OTHER NATURALLY OCCURRING
CC       UNSATURATED FREE FATTY ACIDS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: EXPRESSED MAINLY IN THE CEREBELLUM, SPLEEN,
CC       AND TESTIS.
CC   -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC       CHANNELS.
CC   ---------------------------------------------------------------------
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF196965; AAF75132.1; -.
DR   InterPro; IPR003280; 2poreK_channel.
DR   InterPro; IPR000636; Cation_chan_non_lig.
DR   InterPro; IPR001622; Channel_pore_K.
DR   InterPro; IPR003976; Trek_channel.
DR   Pfam; PF00520; ion_trans; 1.
DR   PRINTS; PR01333; 2POREKCHANEL.
DR   PRINTS; PR01499; TREKCHANNEL.
KW   Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW   Glycoprotein.
FT   DOMAIN        1     71       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     72     92       POTENTIAL.
FT   DOMAIN      154    180       PORE-FORMING 1 (POTENTIAL).
FT   TRANSMEM    182    202       POTENTIAL.
FT   DOMAIN      203    233       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    234    254       POTENTIAL.
FT   DOMAIN      263    294       PORE-FORMING 2 (POTENTIAL).
FT   TRANSMEM    299    319       POTENTIAL.
FT   DOMAIN      320    538       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    144    144       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    147    147       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   538 AA;  59800 MW;  1FF33F0AA52B97E4 CRC64;
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  Query Match             95.1%;  Score 2658.5;  DB 1;  Length 538;
  Best Local Similarity   95.6%;  Pred. No. 4e-159;
  Matches  520;  Conservative    9;  Mismatches    8;  Indels    7;  Gaps    2;

Qy       1 MKFPIETPRKQVNWDPKVAVPAAA-PVCQPKSATNGQPPAPAPTPTPRLSISSRATVVAR 59
           |||||||||||||||||||||||| |||||||||||        | ||||||||||||||
Db       1 MKFPIETPRKQVNWDPKVAVPAAAPPVCQPKSATNGH------HPVPRLSISSRATVVAR 54

Qy      60 MEGTSQGGLQTVMKWKTVVAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLR 119
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      55 MEGASQGGLQTVMKWKTVVAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLR 114

Qy     120 DHVCVSPQELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIA 179
           ||:|||||||||||||||||:|||||:|||||||||||||||||||||||||||||||||
Db     115 DHICVSPQELETLIQHALDADNAGVSPVGNSSNSSSHWDLGSAFFFAGTVITTIGYGNIA 174

Qy     180 PSTEGGKIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVI 239
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     175 PSTEGGKIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVI 234

Qy     240 STILFILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYRE 299
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     235 STILFILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYRE 294

Qy     300 WYKPLVWFWILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRET 359
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     295 WYKPLVWFWILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRET 354

Qy     360 RRRLSVEIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQE 419
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     355 RRRLSVEIHDKLQRAATIRSMERRRLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQE 414

Qy     420 SINNRPNNLRLKGPEQLNKHGQGASEDNIINKFGSTSRLTKRKNKDLKKTLPEDVQKIYK 479
           |||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
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Db    415 SINNRPNNLRLKGPEQLNKHGQGASEDNIINKFGSTSKLTKRKNKDLKKTLPEDVQKIYK 474

Qy    480 TFRNYSLDEEKKEEETEKMCNSDNSSTAMLTDCIQQHAELENGMIPTDTKDREPENNSLL 539
          ||||||||||||||:|||||||||||||||||:|||| ||:||||:| |||||  ||||||
Db    475 TFRNYSLDEEKKEDETEKMCNSDNSSTAMLTECIQQQAEMENGMVPMDTKDQGLENNSLL 534

Qy    540 EDRN 543
          ||||
Db    535 EDRN 538


RESULT   3
CIW2_MOUSE
ID   CIW2_MOUSE     STANDARD;      PRT;   411 AA.
AC   P97438;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Potassium channel subfamily K member 2 (Outward rectifying potassium
DE   channel protein TREK-1) (Two-pore potassium channel TPKC1) (TREK-1 K+
DE   channel subunit).
GN   KCNK2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RC   TISSUE=Brain;
RX   MEDLINE=97157476; PubMed=9003761;
RA   Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,
RA   Lazdunski M.;
RT   "Cloning, functional expression and brain localization of a novel
RT   unconventional outward rectifier K+ channel.";
RL   EMBO J. 15:6854-6862(1996).
RN   [2]
RP   REVISIONS.
RC   TISSUE=Brain;
RA   Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,
RA   Lazdunski M.;
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   ACTIVATION.
RX   MEDLINE=99254548; PubMed=10321245;
RA   Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT   "Inhalational anesthetics activate two-pore-domain background K+
RT   channels.";
RL   Nat. Neurosci. 2:422-426(1999).
CC   -!- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
CC   -!- SUBUNIT: HOMODIMER (POTENTIAL).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN AND LUNG. ALSO
CC       DETECTED IN KIDNEY, HEART AND SKELETAL MUSCLE. NOT DETECTED IN
CC       LIVER. IN THE BRAIN, HIGHEST EXPRESSION IN OLFACTORY BULB,
CC       HIPPOCAMPUS AND CEREBELLUM.
CC   -!- MISCELLANEOUS: INHIBITED BY BARIUM. ACTIVATED BY VOLATILE GENERAL
CC       ANAESTHETICS SUCH AS CHLOROFORM, DIETHYL ETHER, HALOTHANE AND
CC       ISOFLURANE.
CC   -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC       CHANNELS.
CC   ----------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U73488; AAC53005.2; -.
DR   MGD; MGI:109366; Kcnk2.
DR   InterPro; IPR003280; 2poreK_channel.
DR   InterPro; IPR000636; Cation_chan_non_lig.
DR   InterPro; IPR001622; Channel_pore_K.
DR   InterPro; IPR003976; Trek_channel.
DR   Pfam; PF00520; ion_trans; 1.
DR   PRINTS; PR01333; 2POREKCHANEL.
DR   PRINTS; PR01499; TREKCHANNEL.
KW   Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW   Glycoprotein.
FT   DOMAIN        1     46       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     47     67       POTENTIAL.
FT   DOMAIN      129    155       PORE-FORMING 1 (POTENTIAL).
FT   TRANSMEM    157    177       POTENTIAL.
FT   DOMAIN      178    207       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    208    228       POTENTIAL.
FT   DOMAIN      238    268       PORE-FORMING 2 (POTENTIAL).
FT   TRANSMEM    273    293       POTENTIAL.
FT   DOMAIN      294    411       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      378    411       ESSENTIAL FOR CHLOROFORM AND HALOTHANE
FT                                SENSITIVITY.
FT   DOMAIN      354    411       REQUIRED FOR BASAL CHANNEL ACTIVITY.
FT   CARBOHYD     95     95       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    119    119       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   411 AA;  45297 MW;  8F976DDD103EFA05 CRC64;


  Query Match             44.8%;  Score 1251.5;  DB 1;  Length 411;
  Best Local Similarity   64.3%;  Pred. No. 2.5e-71;
  Matches  247;  Conservative   54;  Mismatches   66;  Indels   17;  Gaps    5;

Qy     22 AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI 80
          ||  :  ||||         |    |||| ||: ||:| |:|  |      |||||||  |
Db      2 AAPDLLDPKSA--------AQNSKPRLSFSSKPTVLASRVESDS---AINVMKWKTVSTI 50

Qy     81 FVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD 140
          |:|||:||: |  ||:|||| | ||: || ::|  |:  | ||:  ||: |||  : |
Db     51 FLVVVLYLIIGAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAI 110

Qy    141 NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF 200
          |||: |:|||||  |||||||:||||||||||||:|||:| ||||||||:||: |||||
Db    111 NAGIIPLGNSSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLF 170

Qy    201 GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF 260
          ||||||:|||||||||| ||:||  | |  |||||||:||||:||| ||::|| :|||||
Db    171 GFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAVIF 230

Qy    261 KYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL 320
          |:|||||:||::|||||:||||:||||:|||| : | | ::|||:||||||||||||||||
Db    231 KHIEGWSALDAIYFVVITLTTIGFGDYVAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVL 289

Qy    321 SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM 380
          |||||||||:|||||||||| :|||||| |||||||:|||||||||||:|| ||| ::
Db    290 SMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSV--- 346

Qy    381 ERRRLGLDQRAHSLDMLSPEKRSV 404
           :|:|  :   :    |:| :|::
Db    347 -KRKLSAELAGNHNQELTPCRRTL 369


RESULT   4
CIW2_HUMAN
ID   CIW2_HUMAN     STANDARD;      PRT;   426 AA.
AC   O95069; Q9UNE3;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Potassium channel subfamily K member 2 (Outward rectifying potassium
DE   channel protein TREK-1) (TREK-1 K+ channel subunit) (Two-pore
DE   potassium channel TPKC1).
GN   KCNK2 OR TREK1 OR TREK.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
```

```
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99254548; PubMed=10321245;
RA   Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT   "Inhalational anesthetics activate two-pore-domain background K+
RT   channels.";
RL   Nat. Neurosci. 2:422-426(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Price L.A., Hellings S.E., Hayashi J.H., Pausch M.H.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: OUTWARD RECTIFYING POTASSIUM CHANNEL.
CC   -!- SUBUNIT: HOMODIMER (POTENTIAL).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- MISCELLANEOUS: ACTIVATED BY VOLATILE GENERAL ANAESTHETICS SUCH AS
CC       CHLOROFORM, HALOTHANE AND ISOFLURANE.
CC   -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC       CHANNELS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF129399; AAD47569.1; -.
DR   EMBL; AF004711; AAD01203.1; -.
DR   MIM; 603219; -.
DR   InterPro; IPR003280; 2poreK_channel.
DR   InterPro; IPR000636; Cation_chan_non_lig.
DR   InterPro; IPR001622; Channel_pore_K.
DR   InterPro; IPR003976; Trek_channel.
DR   Pfam; PF00520; ion_trans; 1.
DR   PRINTS; PR01333; 2POREKCHANEL.
DR   PRINTS; PR01499; TREKCHANNEL.
KW   Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW   Glycoprotein.
FT   DOMAIN        1     61       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     62     82       POTENTIAL.
FT   DOMAIN      144    170       PORE-FORMING 1 (POTENTIAL).
FT   TRANSMEM    172    192       POTENTIAL.
FT   DOMAIN      193    223       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    224    244       POTENTIAL.
FT   DOMAIN      253    283       PORE-FORMING 2 (POTENTIAL).
FT   TRANSMEM    288    308       POTENTIAL.
FT   DOMAIN      309    426       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      378    426       ESSENTIAL FOR CHLOROFORM AND HALOTHANE
FT                                SENSITIVITY (BY SIMILARITY).
FT   DOMAIN      354    426       REQUIRED FOR BASAL CHANNEL ACTIVITY (BY
FT                                SIMILARITY).
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    134    134       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT      2     16       MISSING (IN REF. 2).
FT   CONFLICT    309    311       RLV -> DWL (IN REF. 2).
FT   CONFLICT    391    391       S -> N (IN REF. 2).
FT   CONFLICT    411    411       A -> T (IN REF. 2).
SQ   SEQUENCE   426 AA;  47016 MW;  2ABA2336D4009F4E CRC64;


  Query Match             43.6%;  Score 1218.5;  DB 1;  Length 426;
  Best Local Similarity   62.8%;  Pred. No. 3.1e-69;
  Matches  241;  Conservative   58;  Mismatches   68;  Indels   17;  Gaps    5;

Qy      22 AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI 80
           ||  :  ||||         |    |||| |:: ||:| |:|  :      |||||||  |
Db      17 AAPDLLDPKSA--------AQNSKPRLSFSTKPTVLASRVESDT---TINVMKWKTVSTI 65

Qy      81 FVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD 140
           |:|||:||: |  ||:|||| | ||: || ::|  |:  | ||:  ||: |||  : |
Db      66 FLVVVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAI 125

Qy     141 NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF 200
           |||: |:||:||  |||||||:||||||||||||:|||:| |||||||||:||: |||||
Db     126 NAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLF 185

Qy     201 GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF 260
           ||||||:|||||||||| ||:||  | |  |||||||:||||:||| ||::|| :||:||
Db     186 GFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIF 245

Qy     261 KYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL 320
           |:||||:||::|||||:||||:||||:|||| : | | ::|||:||||||||||||||||
Db     246 KHIEGWSALDAIYFVVITLTTIGFGDYVAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVL 304

Qy     321 SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM 380
           |||| :||:|||||||||| :|||||| |||||||:|||||||||:|| ||| :|
Db     305 SMIGRLVRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSI--- 361

Qy     381 ERRRLGLDQRAHSLDMLSPEKRSV 404
           :|:|  :   :    |:| :|::
Db     362 -KRKLSAELAGNHNQELTPCRRTL 384


RESULT   5
CIW4_HUMAN
ID   CIW4_HUMAN     STANDARD;      PRT;   393 AA.
AC   Q9NYG8;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Potassium channel subfamily K member 4 (TWIK-related arachidonic acid-
DE   stimulated potassium channel protein) (TRAAK).
GN   KCNK4 OR TRAAK.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=20499203; PubMed=11042359;
RA   Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M.,
RA   Kelsell R.E., Murdock P.R., Randall A.D., Rennie G.I., Gloger I.S.;
RT   "Cloning, localisation and functional expression of a novel human,
RT   cerebellum specific, two pore domain potassium channel.";
RL   Brain Res. Mol. Brain Res. 82:74-83(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Frontal cortex;
RA   Gray A.T.;
RT   "Assignment of KCNK4 encoding the human potassium channel TRAAK to
RT   chromosome 11.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20231699; PubMed=10767409;
RA   Lesage F., Maingret F., Lazdunski M.;
RT   "Cloning and expression of human TRAAK, a polyunsaturated fatty
RT   acids-activated and mechano-sensitive K(+) channel.";
RL   FEBS Lett. 471:137-140(2000).
CC   -!- FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING
CC       POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED AT HIGH
CC       EXTERNAL K+ CONCENTRATIONS (BY SIMILARITY).
CC   -!- SUBUNIT: HOMODIMER (POTENTIAL).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC       CHANNELS.
CC   ---------------------------------------------------------------------
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
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CC   ----------------------------------------------------------------------
DR   EMBL; AF248242; AAG31731.1; -.
DR   EMBL; AF247042; AAF64062.1; ALT_INIT.
DR   MIM; 605720; -.
DR   InterPro; IPR003280; 2poreK_channel.
DR   InterPro; IPR000636; Cation_chan_non_lig.
DR   InterPro; IPR001622; Channel_pore_K.
DR   InterPro; IPR002958; Occludin.
DR   Pfam; PF00520; ion_trans; 1.
DR   Pfam; PF02168; Occludin; 1.
DR   PRINTS; PR01333; 2POREKCHANEL.
KW   Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW   Glycoprotein.
FT   DOMAIN        1      3       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      4     24       POTENTIAL.
FT   DOMAIN       89    113       PORE-FORMING 1 (POTENTIAL).
FT   TRANSMEM    118    138       POTENTIAL.
FT   DOMAIN      140    171       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    172    192       POTENTIAL.
FT   DOMAIN      197    221       PORE-FORMING 2 (POTENTIAL).
FT   TRANSMEM    234    254       POTENTIAL.
FT   DOMAIN      255    393       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     78     78       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     82     82       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    328    328       P -> L (IN REF. 2).
SQ   SEQUENCE   393 AA;  42704 MW;  7F18E53A0A9AD57D CRC64;


  Query Match             29.1%;  Score 812.5;  DB 1;  Length 393;
  Best Local Similarity   53.8%;  Pred. No. 6.6e-44;
  Matches  157;  Conservative   53;  Mismatches   77;  Indels    5;  Gaps    3;

Qy      72 MKWKTVVAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELET 131
           |:  |::|:  :|::|||:| |||||||| |   :  :   : :||| | ||| |||
Db       1 MRSTTLLALLALVLLYLVSGALVFRALEQPHEQQAQRELGEVREKFLRAHPCVSDQELGL 60

Qy     132 LIQHALDADNAGVSPIGNSSNNSSH--WDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFC 189
           ||:   ||   |  |  ||::|||| |||||||||:||:|||||||:|  |: |::||
Db      61 LIKEVADALGGGADPETNSTSNSSHSAWDLGSAFFFSGTIITTIGYGNVALRTDAGRLFC 120

Qy     190 ILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGC 249
           | ||: |||||| ||||:||:||:     |  :| :| |  |    :||:| :||:| ||
Db     121 IFYALVGIPLFGILLAGVGDRLGSSLRHGIGHIEAIFLKWHVPPELVRVLSAMLFLLIGC 180

Qy     250 IVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWI 309
           ::||  |  :| |:| |: ||:||||:||||||||||:||| :   :    |:|||||||
Db     181 LLFVLTPTFVFCYMEDWSKLEAIYFVIVTLTTVGFGDYVAGADPRQD-SPAYQPLVWFWI 239

Qy     310 LVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRR 361
           |:||||||:||: ||:||||:|::|: |:| : | || |   |||  | |:|
Db     240 LLGLAYFASVLTTIGNWLRVVSRRTRAEMGGLTAQAASWTGTVTA--RVTQR 289


RESULT   6
CIW4_MOUSE
ID   CIW4_MOUSE     STANDARD;      PRT;   398 AA.
AC   O88454;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Potassium channel subfamily K member 4 (TWIK-related arachidonic acid-
DE   stimulated potassium channel protein) (TRAAK).
GN   KCNK4 OR TRAAK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=98292450; PubMed=9628867;
RA   Fink M., Lesage F., Duprat F., Heurteaux C., Reyes R., Fosset M.,
RA   Lazdunski M.;
RT   "A neuronal two P domain K+ channel stimulated by arachidonic acid and
RT   polyunsaturated fatty acids.";
RL   EMBO J. 17:3297-3308(1998).
RN   [2]
RP   ACTIVATION.
RX   MEDLINE=99254548; PubMed=10321245;
RA   Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT   "Inhalational anesthetics activate two-pore-domain background K+
RT   channels.";
RL   Nat. Neurosci. 2:422-426(1999).
CC   -!- FUNCTION: VOLTAGE INSENSITIVE, INSTANTANEOUS, OUTWARDLY RECTIFYING
CC       POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS REVERSED AT HIGH
CC       EXTERNAL K+ CONCENTRATIONS.
CC   -!- SUBUNIT: HOMODIMER (POTENTIAL).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND
CC       2/TRAAKT/TRUNCATED; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN, SPINAL CORD AND EYE. NOT
CC       DETECTED IN HEART, SKELETAL MUSCLE, LIVER, LUNGS, KIDNEY AND
CC       TESTIS.
CC   -!- MISCELLANEOUS: ACTIVATED BY ARACHIDONIC ACID AND OTHER UNSATURATED
CC       FATTY ACIDS. NOT AFFECTED BY VOLATILE GENERAL ANAESTHETICS SUCH AS
CC       CHLOROFORM, DIETHYL ETHER, HALOTHANE AND ISOFLURANE.
CC   -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC       CHANNELS.
CC   ----------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF056492; AAC40181.1; -.
DR   MGD; MGI:1298234; Kcnk4.
DR   InterPro; IPR003280; 2poreK_channel.
DR   InterPro; IPR000636; Cation_chan_non_lig.
DR   InterPro; IPR001622; Channel_pore_K.
DR   Pfam; PF00520; ion_trans; 1.
DR   PRINTS; PR01333; 2POREKCHANEL.
KW   Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW   Glycoprotein; Alternative splicing.
FT   DOMAIN        1      3       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      4     24       POTENTIAL.
FT   DOMAIN       89    113       PORE-FORMING 1 (POTENTIAL).
FT   TRANSMEM    119    139       POTENTIAL.
FT   DOMAIN      140    171       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    172    192       POTENTIAL.
FT   DOMAIN      198    222       PORE-FORMING 2 (POTENTIAL).
FT   TRANSMEM    235    255       POTENTIAL.
FT   DOMAIN      256    398       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     81     81       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     84     84       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC     63     67       KLLVE -> KAMAI (IN ISOFORM 2).
FT   VARSPLIC     68    398       MISSING (IN ISOFORM 2).
SQ   SEQUENCE   398 AA;  43051 MW;  478A834B7B7AEC92 CRC64;


  Query Match             28.3%;  Score 790;  DB 1;  Length 398;
  Best Local Similarity   51.9%;  Pred. No. 1.7e-42;
  Matches  152;  Conservative   55;  Mismatches   80;  Indels    6;  Gaps    3;

Qy      72 MKWKTVVAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELET 131
           |:  |::|:  :|::|||:| |||:||||| |   :  :   : :||||| ||| : ||
Db       1 MRSTTLLALLALVLLYLVSGALVFQALEQPHEQQAQKKMDHGRDQFLRDHPCVSQKSLED 60

Qy     132 LIQHALDADNAGVSP---IGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIF 188
           |:  ::|   | :|     ||||:|| |:|||||||:||:|||||||||   |: |::|
Db      61 FIKLLVEALGGGANPETSWTNSSNHSSAWNLGSAFFFSGTIITTIGYGNIVLHTDAGRLF 120

Qy     189 CILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAG 248
           || ||: |||||| ||||:||:||:   : |  :| :| |  |    :| :| :||:| |
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Db    121 CIFYALVGIPLFGMLLAGVGDRLGSSLRRGIGHIEAIFLKWHVPPGLVRSLSAVLFLLIG 180

Qy    249 CIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFW 308
          |::||  |  :| |:| |: ||:||||:||||||||||:| |   | |    |:||||||
Db    181 CLLFVLTPTFVFSYMESWSKLEAIYFVIVTLTTVGFGDYVPGDGTGQN-SPAYQPLVWFW 239

Qy    309 ILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRR 361
          || ||||||:||: ||:||| :|:::|: |:| : | || |   |||  | |:|
Db    240 ILFGLAYFASVLTTIGNWLRAVSRRTRAEMGGLTAQAASWTGTVTA--RVTQR 290


RESULT   7
CIW5_HUMAN
ID   CIW5_HUMAN     STANDARD;      PRT;   499 AA.
AC   O95279;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Potassium channel subfamily K member 5 (Acid-sensitive potassium
DE   channel protein TASK-2) (TWIK-related acid-sensitive K+ channel 2).
GN   KCNK5 OR TASK2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=99030343; PubMed=9812978;
RA   Reyes R., Duprat F., Lesage F., Fink M., Salinas M., Farman N.,
RA   Lazdunski M.;
RT   "Cloning and expression of a novel pH-sensitive two pore domain K+
RT   channel from human kidney.";
RL   J. Biol. Chem. 273:30863-30869(1998).
CC   -!- FUNCTION: PH DEPENDENT, VOLTAGE INSENSITIVE, OUTWARDLY RECTIFYING
CC       POTASSIUM CHANNEL. OUTWARD RECTIFICATION IS LOST AT HIGH EXTERNAL
CC       K+ CONCENTRATIONS.
CC   -!- SUBUNIT: HOMODIMER (POTENTIAL).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: ABUNDANT EXPRESSION IN KIDNEY, ALSO DETECTED
CC       IN LIVER, PLACENTA AND SMALL INTESTINE. IN THE KIDNEY, EXPRESSION
CC       IS RESTRICTED TO THE DISTAL TUBULES AND COLLECTING DUCTS. NOT
CC       EXPRESSED IN PROXIMAL TUBULES OR GLOMERULI.
CC   -!- MISCELLANEOUS: INHIBITED BY QUININE, QUINIDINE AND EXTERNAL
CC       ACIDIFICATION.
CC   -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC       CHANNELS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF084830; AAC79458.1; -.
DR   MIM; 603493; -.
DR   InterPro; IPR003280; 2poreK_channel.
DR   InterPro; IPR000636; Cation_chan_non_lig.
DR   InterPro; IPR001622; Channel_pore_K.
DR   Pfam; PF00520; ion_trans; 1.
DR   PRINTS; PR01333; 2POREKCHANEL.
KW   Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW   Glycoprotein.
FT   DOMAIN       1      7       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     8     26       POTENTIAL.
FT   DOMAIN      85    112       PORE-FORMING 1 (POTENTIAL).
FT   TRANSMEM   113    133       POTENTIAL.
FT   DOMAIN     134    157       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   158    180       POTENTIAL.
FT   DOMAIN     190    215       PORE-FORMING 2 (POTENTIAL).
FT   TRANSMEM   230    250       POTENTIAL.
FT   DOMAIN     251    325       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    77     77       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   499 AA;  55130 MW;  E871A7A4823DDA00 CRC64;


  Query Match             17.3%;  Score 483;  DB 1;  Length 499;
  Best Local Similarity   25.8%;  Pred. No. 3.5e-23;
  Matches  131;  Conservative   81;  Mismatches  185;  Indels  110;  Gaps   14;

Qy     84 VVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDADNAG 143
          :: ||  |  :|  ||:|     |     :|   |::  |:  : |: :::   ||   |
Db     12 IIFYLAIGAAIFEVLEEPHWKEAKKNYYTQKLHLLKEFPCLGQEGLDKILEVVSDAAGQG 71

Qy    144 VSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLFGFL 203
          |:  || : |  :|:  :|  || |||||||||:|| |  |::||: | :||:||
Db     72 VAITGNQTFN--NWNWPNAMIFAATVITTIGYGNVAPKTPAGRLFCVFYGLFGVPL---C 126

Qy    204 LAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIFKYI 263
          |  |   || ||    |: :   |: ||  | ::  |::||: | :| : ||  :|
Db    127 LTWI-SALGKFFGGRAKRLGQFLTKRGVSLRKAQITCTVIFIVWGVLVHLVIPPFVFMVT 185

Qy    264 EGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVLSMI 323
          |||  :| :|:  :|:::|:|||||||| |   ||   |:  |  || :|||
Db    186 EGWNYIEGLYYSFITISTIGFGDFVAGVNPSANYHALYRYFVELWIYLGLA--------- 236

Qy    324 GDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSMERR 383
            || :                || :          : ||:|  ::     :   ||
Db    237 --WLSLF--------------VNWKVS----------MFVEVHKAIK-----KRRRRR 263

Qy    384 RLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNLRLK----------GP 433
          :   :  ||  |  : :    ::  | :  :|: |:   :  |                ||
Db    264 KESFESSPHSRKALQVKGSTASKDVNIFSFLSKKEETYNDLIKQIGKKAMKTSGGGETGP 323

Qy    434 -EQLNKHGQG------------------ASEDNIINKFGSTSRLTKRKNKDLKKTLPED 473
           |  | |                  : : :     |  :::  :::     |||
Db    324 GPGLGPQGGGLPALPPSLVPLVVYSKNRVPTLEEVSQTLRSKGHVSRSPDEEAVARAPED 383

Qy    474 VQKIYKTFRNYSLDEEKKEEE--------------------TEKMCNSDNSSTAMLTDC 512
            : | |  ||   :| |                       ||   : : :| : | |
Db    384 SSPAPEVFMN-QLDRISEECEPWDAQDYHPLIFQDASITFVNTEAGLSDEETSKSSLEDN 442

Qy    513 I------QQHAE----LENGMIPTDTK 529
          :      || ||    |  |  |: ::
Db    443 LAGEESPQQGAEAKAPLNMGEFPSSSE 469


RESULT   8
CIW1_HUMAN
ID   CIW1_HUMAN     STANDARD;      PRT;   336 AA.
AC   O00180; Q13307;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Potassium channel subfamily K member 1 (Inward rectifying potassium
DE   channel protein TWIK-1) (Potassium channel KCNO1).
GN   KCNK1 OR TWIK1 OR HOHO1 OR KCNO1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., FUNCTION, AND MUTAGENESIS OF THR-161.
RC   TISSUE=Kidney;
RX   MEDLINE=96183184; PubMed=8605869;
RA   Lesage F., Guillemare E., Fink M., Duprat F., Lazdunski M., Romey G.,
RA   Barhanin J.;
RT   "TWIK-1, a ubiquitous human weakly inward rectifying K+ channel with a
RT   novel structure.";
RL   EMBO J. 15:1004-1011(1996).
RN   [2]
RP   SEQUENCE FROM N.A., AND REVIEW.
RC   TISSUE=Brain;
RX   MEDLINE=98122696; PubMed=9462864;
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RA   Goldstein S.A.N., Wang K.-W., Ilan N., Pausch M.H.;
RT   "Sequence and function of the two P domain potassium channels:
RT   implications of an emerging superfamily.";
RL   J. Mol. Med. 76:13-20(1998).
RN   [3]
RP   SEQUENCE FROM N.A..
RX   MEDLINE=98026667; PubMed=9362344;
RA   Orias M., Velazquez H., Tung F., Lee G., Desir G.V.;
RT   "Cloning and localization of a double-pore K channel, KCNK1: exclusive
RT   expression in distal nephron segments.";
RL   Am. J. Physiol. 273:F663-F666(1997).
CC   -!- FUNCTION: WEAKLY INWARD RECTIFYING POTASSIUM CHANNEL.
CC   -!- SUBUNIT: HOMODIMER (POTENTIAL).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGH LEVELS IN HEART AND
CC       BRAIN AND LOWER LEVELS IN PLACENTA, LUNG, LIVER AND KIDNEY.
CC   -!- MISCELLANEOUS: INHIBITED BY BARIUM, QUININE, QUINIDINE AND
CC       INTERNAL ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.
CC   -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC       CHANNELS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U33632; AAB01688.1; -.
DR   EMBL; U76996; AAB97878.1; -.
DR   EMBL; U90065; AAB51147.1; -.
DR   MIM; 601745; -.
DR   InterPro; IPR003280; 2poreK_channel.
DR   InterPro; IPR000636; Cation_chan_non_lig.
DR   InterPro; IPR001622; Channel_pore_K.
DR   InterPro; IPR001779; TWIK1_channel.
DR   Pfam; PF00520; ion_trans; 1.
DR   PRINTS; PR01333; 2POREKCHANEL.
DR   PRINTS; PR01096; TWIK1CHANNEL.
KW   Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW   Glycoprotein.
FT   DOMAIN        1     20       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     21     41       POTENTIAL.
FT   DOMAIN      104    130       PORE-FORMING 1 (POTENTIAL).
FT   TRANSMEM    133    153       POTENTIAL.
FT   DOMAIN      154    177       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    178    198       POTENTIAL.
FT   DOMAIN      212    238       PORE-FORMING 2 (POTENTIAL).
FT   TRANSMEM    247    267       POTENTIAL.
FT   DOMAIN      268    336       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     95     95       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   MUTAGEN     161    161       T->A: NO EFFECT ON CHANNEL ACTIVITY.
SQ   SEQUENCE   336 AA;  38143 MW;  2A41D9501323215D CRC64;


  Query Match             14.4%;  Score 403;  DB 1;  Length 336;
  Best Local Similarity   33.2%;  Pred. No. 2.2e-18;
  Matches   95;  Conservative   53;  Mismatches  104;  Indels   34;  Gaps    9;

Qy      81 FVVV--VVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALD 138
           |:|:  ::||| | :|| ::| |:|   :  :   |  || :| |:| |:||  :   |:
Db      25 FLVLGYLLYLVFGAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEQQLEQFLGRVLE 84

Qy     139 ADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIP 198
           | | ||| : |:| |  :||  || ||| ||::| |||:  | ::||| |||:|:: |||
Db      85 ASNYGVSVLSNASGN-WNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIP 143

Qy     199 LFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQV---------SQTKIRVISTIL--FILA 247
                 |  :          : |:     :: |         |:  : ::  :|  |:
Db     144 FTLLFLTAV-----------VQRITVHVTRRPVLYFHIRWGFSKQVVAIVHAVLLGFVTV 192

Qy     248 GCIVFVTIPAVIFKYIE-GWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVW 306
           |  |  ||| :|  :|  |  ||| ||  ::|:|:| ||:| |      :|| ||  :
Db     193 SCFFF--IPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYKIGIT 250

Qy     307 FWILVGLAYFAAVLSMIGDWLRVLSK-----KTKEEVGEIKAHAAE 347
           ::|:||     ||    : |  | |       |::  | : |  |
Db     251 CYLLLGLIAMLVVLETFCE-LHELKKFRKMFYVKKDKDEDQVHIIE 295


RESULT   9
CIW1_MOUSE
ID   CIW1_MOUSE     STANDARD;      PRT;   336 AA.
AC   O08581;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Potassium channel subfamily K member 1 (Inward rectifying potassium
DE   channel protein TWIK-1).
GN   KCNK1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97165959; PubMed=9013852;
RA   Lesage F., Lauritzen I., Duprat F., Reyes R., Fink M., Heurteaux C.,
RA   Lazdunski M.;
RT   "The structure, function and distribution of the mouse TWIK-1 K+
RT   channel.";
RL   FEBS Lett. 402:28-32(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SVJ; TISSUE=Liver;
RX   MEDLINE=98218573; PubMed=9559671;
RA   Arrighi I., Lesage F., Scimeca J.-C., Carle G.F., Barhanin J.;
RT   "Structure, chromosome localization, and tissue distribution of the
RT   mouse twik K+ channel gene.";
RL   FEBS Lett. 425:310-316(1998).
CC   -!- FUNCTION: WEAK INWARDLY RECTIFYING POTASSIUM CHANNEL.
CC   -!- SUBUNIT: HOMODIMER (POTENTIAL).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST EXPRESION IN BRAIN,
CC       KIDNEY, THYROID, SALIVARY GLAND, ADRENAL GLAND, PROSTATE,
CC       EPIDIDYMIS, UTERUS, PLACENTA, COLON AND JEJUNUM. MODERATE
CC       EXPRESSION IN EYES, PITUITARY, PANCREAS, SMOOTH MUSCLE, TESTIS AND
CC       OVARY. VERY LOW LEVELS IN LUNG, AORTA, LIVER, HEART, SKELETAL
CC       MUSCLE, THYMUS AND SPLEEN. IN THE BRAIN, HIGHEST EXPRESSION IN
CC       CEREBELLAR GRANULE CELLS, BRAINSTEM, HIPPOCAMPUS AND CEREBRAL
CC       CORTEX.
CC   -!- DEVELOPMENTAL STAGE: EXPRESSION DETECTED AS EARLY AS 7 DAYS POST
CC       CONCEPTION. EXPRESSION INCREASES FROM 2-8 DAYS AFTER BIRTH AND
CC       STABILIZES AFTER DAY 8.
CC   -!- MISCELLANEOUS: INHIBITED BY QUININE, BARIUM, AND INTERNAL
CC       ACIDIFICATION. ACTIVATED BY PROTEIN KINASE C.
CC   -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC       CHANNELS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF033017; AAC16973.1; -.
DR   MGD; MGI:109322; Kcnk1.
DR   InterPro; IPR003280; 2poreK_channel.
DR   InterPro; IPR000636; Cation_chan_non_lig.
DR   InterPro; IPR001622; Channel_pore_K.
DR   InterPro; IPR001779; TWIK1_channel.
DR   Pfam; PF00520; ion_trans; 1.
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DR   PRINTS; PR01333; 2POREKCHANEL.
DR   PRINTS; PR01096; TWIK1CHANNEL.
KW   Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW   Glycoprotein.
FT   DOMAIN        1     20       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     21     41       POTENTIAL.
FT   DOMAIN      104    130       PORE-FORMING 1 (POTENTIAL).
FT   TRANSMEM    133    153       POTENTIAL.
FT   DOMAIN      154    177       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    178    198       POTENTIAL.
FT   DOMAIN      212    238       PORE-FORMING 2 (POTENTIAL).
FT   TRANSMEM    247    267       POTENTIAL.
FT   DOMAIN      268    336       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     95     95       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   336 AA;  38275 MW;  A996060A18266FD4 CRC64;


  Query Match             14.0%;  Score 390.5;  DB 1;  Length 336;
  Best Local Similarity   33.7%;  Pred. No. 1.3e-17;
  Matches   94;  Conservative   49;  Mismatches   99;  Indels   37;  Gaps    9;

Qy      81 FVVV--VVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALD 138
           |:|:  ::||| | :|| : | |:|    :  :    |  || :| |:|  :||  :   |:
Db      25 FLVLGYLLYLVFGAVVFSSEELPYEDLLRQELRKLKRRFLEEHECLSEPQLEQFLGRVLE 84

Qy     139 ADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIP 198
           | | ||| : |:| |  :||  || ||| ||::| |||:  | ::|||| |||:|:: |||
Db      85 ASNYGVSVLSNASGN-WNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIP 143

Qy     199 LFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQV---------SQTKIRVISTIL--FILA 247
                 |  :          : ||     :: |         |:  : ::  :|  |:
Db      144 FTLLFLTAL----------VQRVTVHVTRRPVLYFHIRWGFSKQVVAIVHAVLLGFVTV 192

Qy     248 GCIVFVTIPAVIFKYIE-GWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVW 306
           |  |  ||| :|  :|  |  ||| ||  ::|:|:| ||:| |      :|| ||  :
Db      193 SCFFF--IPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYKIGIT 250

Qy     307 FWILVGLAYFAAVLSMIGDWLRVLS--------KKTKEE 337
            ::|:||     ||    : |  |          || |:|
Db      251 CYLLLGLITMLVVLETFCE-LHELKKFRKMFYVKKDKDE 288


RESULT  10
CIW3_MOUSE
ID   CIW3_MOUSE     STANDARD;      PRT;   409 AA.
AC   O35111; O35163;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Potassium channel subfamily K member 3 (Acid-sensitive potassium
DE   channel protein TASK) (TWIK-related acid-sensitive K+ channel)
DE   (Cardiac two-pore background K+ channel) (cTBAK-1).
GN   KCNK3 OR TASK OR CTBAK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=98165556; PubMed=9506712;
RA   Kim D., Fujita A., Horio Y., Kurachi Y.;
RT   "Cloning and functional expression of a novel cardiac two-pore
RT   background K+ channel (cTBAK-1).";
RL   Circ. Res. 82:513-518(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=20287574; PubMed=10748056;
RA   Lopes C.M., Gallagher P.G., Buck M.E., Butler M.H., Goldstein S.A.;
RT   "Proton block and voltage gating are potassium-dependent in the
RT   cardiac leak channel Kcnk3.";
RL   J. Biol. Chem. 275:16969-16978(2000).
RN   [3]
RP   SEQUENCE OF 4-409 FROM N.A.
RX   MEDLINE=97459932; PubMed=9312005;
RA   Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.;
RT   "TASK, a human background K+ channel to sense external pH variations
RT   near physiological pH.";
RL   EMBO J. 16:5464-5471(1997).
CC   -!- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM
CC       CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM
CC       ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN
CC       OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.
CC       WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD
CC       (BY SIMILARITY).
CC   -!- SUBUNIT: HOMODIMER (POTENTIAL).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: VERY STRONG EXPRESSION IN HEART, ALSO DETECTED
CC       IN KIDNEY, BRAIN, SKIN, TESTIS, LUNG, SKELETAL MUSCLE, SMALL
CC       INTESTINE AND STOMACH. NOT DETECTED IN LIVER, THYMUS OR SPLEEN.
CC   -!- MISCELLANEOUS: INACTIVATED BY BARIUM.
CC   -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC       CHANNELS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB008537; BAA25436.1; -.
DR   EMBL; AF241798; AAF81418.1; -.
DR   EMBL; AF242508; AAF81418.1; JOINED.
DR   EMBL; AF065162; AAG29339.1; -.
DR   EMBL; AF006824; AAC53367.1; -.
DR   EMBL; AB013345; BAA28349.1; -.
DR   MGD; MGI:1100509; Kcnk3.
DR   InterPro; IPR003280; 2poreK_channel.
DR   InterPro; IPR000636; Cation_chan_non_lig.
DR   InterPro; IPR001622; Channel_pore_K.
DR   InterPro; IPR003092; TASK_channel.
DR   Pfam; PF00520; ion_trans; 1.
DR   PRINTS; PR01333; 2POREKCHANEL.
DR   PRINTS; PR01095; TASKCHANNEL.
KW   Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW   Glycoprotein.
FT   DOMAIN        1      8       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      9     29       POTENTIAL.
FT   DOMAIN       78    101       PORE-FORMING 1 (POTENTIAL).
FT   TRANSMEM    108    128       POTENTIAL.
FT   DOMAIN      129    158       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    159    179       POTENTIAL.
FT   DOMAIN      184    207       PORE-FORMING 2 (POTENTIAL).
FT   TRANSMEM    223    243       POTENTIAL.
FT   DOMAIN      244    409       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     53     53       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT      4      4       Q -> E (IN REF. 3).
FT   CONFLICT    123    123       V -> I (IN REF. 3).
SQ   SEQUENCE   409 AA;  45068 MW;  35236E011AAC5687 CRC64;


  Query Match             12.6%;  Score 352.5;  DB 1;  Length 409;
  Best Local Similarity   32.3%;  Pred. No. 4e-15;
  Matches   93;  Conservative   54;  Mismatches  112;  Indels   29;  Gaps    9;

Qy      72 MKWKTV--VAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSP--- 126
           || : |  :|: |    ||: |  || ||| |  ::  : | : | ||    :|
Db       1 MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPEMIERQRLELRQLE-LRARYNLSEGGY 59

Qy     127 QELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGK 186
           :||| ::   |    |||           |    :|:|| |||||||||: ||||:|||
Db      60 EELERVVLR-LKPHKAGV----------QWRFAGSFYFAITVITTIGYGHAAPSTDGGK 107
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Qy    187 IFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFIL 246
          :||: ||: ||||   :   :|::: |     : | :   |   :   :: : : :|
Db    108 VFCMFYALLGIPLTLVMFQSLGERINTFVRYLLHRAK---RGLGMRHAEVSMANMVLIGF 164

Qy    247 AGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVA-GGNAGINYREWYKPLV 305
            ||  : | |  | | | ||  :: |:  :||||:||||:||   :  :  :  |
Db    165 VSCISTLCIGAAAFSYYERWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFS 224

Qy    306 WFWILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVT 353
          : :|| ||    | |:::   || ::   ::|  :     || :| :|
Db    225 FVYILTGLTVIGAFLNLV--VLRFMTMNAEDEKRD-----AEHRALLT 265


RESULT  11
CIW3_RAT
ID   CIW3_RAT       STANDARD;      PRT;   411 AA.
AC   O54912;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Potassium channel subfamily K member 3 (Acid-sensitive potassium
DE   channel protein TASK) (TWIK-related acid-sensitive K+ channel).
GN   KCNK3 OR TASK.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cerebellum;
RX   MEDLINE=98099797; PubMed=9437008;
RA   Leonoudakis D., Gray A.T., Winegar B.D., Kindler C.H., Harada M.,
RA   Taylor D.M., Chavez R.A., Forsayeth J.R., Yost C.S.;
RT   "An open rectifier potassium channel with two pore domains in tandem
RT   cloned from rat cerebellum.";
RL   J. Neurosci. 18:868-877(1998).
CC   -!- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM
CC       CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM
CC       ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN
CC       OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.
CC       WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD
CC       (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: STRONGEST EXPRESSION IN HEART. MODERATE
CC       EXPRESSION IN LUNG AND BRAIN. LOW LEVELS IN LIVER, KIDNEY AND
CC       SKELETAL MUSCLE.
CC   -!- MISCELLANEOUS: INHIBITED BY EXTRACELLULAR ACIDIFICATION, ZINC,
CC       BUPIVACAINE AND PHENYTOIN. ACTIVATED BY PROTEIN KINASE A.
CC   -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC       CHANNELS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF031384; AAC39952.1; -.
DR   InterPro; IPR003280; 2poreK_channel.
DR   InterPro; IPR000636; Cation_chan_non_lig.
DR   InterPro; IPR001622; Channel_pore_K.
DR   InterPro; IPR003092; TASK_channel.
DR   Pfam; PF00520; ion_trans; 1.
DR   PRINTS; PR01333; 2POREKCHANEL.
DR   PRINTS; PR01095; TASKCHANNEL.
KW   Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW   Glycoprotein.
FT   DOMAIN        1      8       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      9     29       POTENTIAL.
FT   DOMAIN       78    101       PORE-FORMING 1 (POTENTIAL).
FT   TRANSMEM    108    128       POTENTIAL.
FT   DOMAIN      129    158       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    159    179       POTENTIAL.
FT   DOMAIN      184    207       PORE-FORMING 2 (POTENTIAL).
FT   TRANSMEM    223    243       POTENTIAL.
FT   DOMAIN      244    411       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     53     53       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   411 AA;  45276 MW;  D2778016E09E2BF5 CRC64;


  Query Match             12.6%;  Score 352.5;  DB 1;  Length 411;
  Best Local Similarity   32.3%;  Pred. No. 4e-15;
  Matches   93;  Conservative   54;  Mismatches  112;  Indels   29;  Gaps    9;

Qy     72 MKWKTV--VAIFVVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSP--- 126
          || : |  :|: |    ||: |  || |||   |  ::  : | : | ||    :|
Db      1 MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPEMIERQRLELRQLE-LRARYNLSEGGY 59

Qy    127 QELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGK 186
          :||| ::   |    |||            |    :|:|| |||||||||: |||||:|||
Db     60 EELERVVLR-LKPHKAGV----------QWRFAGSFYFAITVITTIGYGHAAPSTDGGK 107

Qy    187 IFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFIL 246
          :||: ||: ||||   :   :|::: |     : | :   |   :   :: : : :|
Db    108 VFCMFYALLGIPLTLVMFQSLGERINTFVRYLLHRAK---RGLGMRHAEVSMANMVLIGF 164

Qy    247 AGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVA-GGNAGINYREWYKPLV 305
            ||  : | |  | | | ||  :: |:  :||||:||||:||   :  :  :  |
Db    165 VSCISTLCIGAAAFSYYERWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFS 224

Qy    306 WFWILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVT 353
          : :|| ||    | |:::   || ::   ::|  :     || :| :|
Db    225 FVYILTGLTVIGAFLNLV--VLRFMTMNAEDEKRD-----AEHRALLT 265


RESULT  12
CIW9_CAVPO
ID   CIW9_CAVPO     STANDARD;      PRT;   365 AA.
AC   Q9JL58;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Potassium channel subfamily K member 9 (Acid-sensitive potassium
DE   channel protein TASK-3) (TWIK-related acid-sensitive K+ channel 3).
GN   KCNK9 OR TASK3.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=20287530; PubMed=10747866;
RA   Rajan S., Wischmeyer E., Liu G.X., Preisig-Mueller R., Daut J.,
RA   Karschin A., Derst C.;
RT   "TASK-3, a novel tandem pore domain acid-sensitive K+ channel. An
RT   extracellular histidine as pH sensor.";
RL   J. Biol. Chem. 275:16650-16657(2000).
CC   -!- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM
CC       CHANNEL PROTEIN.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC       CHANNELS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF212827; AAF63706.1; -.
DR   InterPro; IPR003280; 2poreK_channel.
```

```
DR   InterPro; IPR000636; Cation_chan_non_lig.
DR   InterPro; IPR001622; Channel_pore_K.
DR   InterPro; IPR003092; TASK_channel.
DR   Pfam; PF00520; ion_trans; 1.
DR   PRINTS; PR01333; 2POREKCHANEL.
DR   PRINTS; PR01095; TASKCHANNEL.
KW   Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW   Glycoprotein.
FT   DOMAIN        1      8       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      9     29       POTENTIAL.
FT   DOMAIN       78    101       PORE-FORMING 1 (POTENTIAL).
FT   TRANSMEM    108    128       POTENTIAL.
FT   DOMAIN      129    158       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    159    179       POTENTIAL.
FT   DOMAIN      184    207       PORE-FORMING 2 (POTENTIAL).
FT   TRANSMEM    219    239       POTENTIAL.
FT   DOMAIN      240    365       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     53     53       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   365 AA;  40769 MW;  261DC973FF53AF91 CRC64;


  Query Match             12.5%;  Score 350.5;  DB 1;  Length 365;
  Best Local Similarity   26.9%;  Pred. No. 4.6e-15;
  Matches  112;  Conservative   72;  Mismatches  153;  Indels   79;  Gaps   17;

Qy      72 MKWKTV--VAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQ-- 127
           || : |  :::      ||: |  || |||   |  ::  :  |:   :|    :| :
Db       1 MKKQNVRTLSLIACTFTYLLVGAAVFDALESDHEMREEEKLKAEEIR-IRGKYNISTEDY 59

Qy     128 -ELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGK 186
            :|| :|  : :   |||            |    :|:|| |||||||||: || |: ||
Db      60 RQLELVILQS-EPHRAGV----------QWKFAGSFYFAITVITTIGYGHAAPGTDAGK 107

Qy     187 IFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKV--FRKKQVSQTKIRVISTILF 244
           ||: ||: ||||   :   :|::: |    : |::|   |  :||   :  :
Db     108 AFCMFYAVLGIPLTLVMFQSLGERMNTFVRYLLKRIKKCCGMRNTEVSMENMVTVG---- 163

Qy     245 ILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAG-INYREWYKP 303
             |:  : | |  |   | |:   : |:  :||||:||||:||  : | :  : :|
Db     164 -FFSCMGTLCIGAAAFSQCEEWSFFHAYYYCFITLTTIGFGDYVALQSKGALQRKPFYVA 222

Qy     304 LVWFWILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGE------IKAHAAEWKANVTAEFR 357
           : :|||||    | |:::   || |:  : || ||      :  : :    ::: | |
Db     223 FSFMYILVGLTVIGAFLNLV--VLRFLTMNSDEERGEGEEGAALPGNPSSVVTHISEEAR 280

Qy     358 ETRRRLSVEIHD--KLQRAATIRSMERRRLG---LDQRAHS----LDMLSPE--KRSVFA 406
           : |:|   |  |   :   |  || : :  |     |  ||    :: :||   | |:|
Db     281 QVRQRYRGEGGDLQSVCSCACYRS-QPQNFGATLAPQPLHSISCRIEEISPSTLKNSLF- 338

Qy     407 ALDTGRFKASSQESINNRPNNLRLKGPEQLNKHGQGASEDNIINKFGSTSRLTKRK 462
                                 |  ::    |      :: ||   ||  |:
Db     339 -------------------------PSPISSVSPG------LHSFGDNHRLMLRR 362


RESULT  13
CIW3_HUMAN
ID   CIW3_HUMAN     STANDARD;      PRT;   394 AA.
AC   O14649;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Potassium channel subfamily K member 3 (Acid-sensitive potassium
DE   channel protein TASK) (TWIK-related acid-sensitive K+ channel).
GN   KCNK3 OR TASK.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Kidney;
RX   MEDLINE=97459932; PubMed=9312005;
RA   Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.;
RT   "TASK, a human background K+ channel to sense external pH variations
RT   near physiological pH.";
RL   EMBO J. 16:5464-5471(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RA   Lopes C.M.B., Gallagher P.G., Buck M.E., Butler M.H.,
RA   Goldstein S.A.N.;
RT   "Proton block and voltage-gating are potassium-dependent in the
RT   cardiac leak channel Kcnk3.";
RL   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   ACTIVATION.
RX   MEDLINE=99254548; PubMed=10321245;
RA   Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT   "Inhalational anesthetics activate two-pore-domain background K+
RT   channels.";
RL   Nat. Neurosci. 2:422-426(1999).
CC   -!- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM
CC       CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM
CC       ION CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN
CC       OUTWARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.
CC       WHEN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION IN ADULT. STRONGEST
CC       EXPRESSION IN PANCREAS AND PLACENTA. LOWER EXPRESSION IN BRAIN,
CC       LUNG, PROSTATE, HEART, KIDNEY, UTERUS, SMALL INTESTINE AND COLON.
CC   -!- MISCELLANEOUS: INHIBITED BY EXTERNAL ACIDIFICATION. ACTIVATED BY
CC       HALOTHANE AND ISOFLURANE.
CC   -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC       CHANNELS.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF006823; AAC51777.1; -.
DR   EMBL; AF065163; AAG29340.1; -.
DR   MIM; 603220; -.
DR   InterPro; IPR003280; 2poreK_channel.
DR   InterPro; IPR000636; Cation_chan_non_lig.
DR   InterPro; IPR001622; Channel_pore_K.
DR   InterPro; IPR003092; TASK_channel.
DR   Pfam; PF00520; ion_trans; 1.
DR   PRINTS; PR01333; 2POREKCHANEL.
DR   PRINTS; PR01095; TASKCHANNEL.
KW   Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW   Glycoprotein.
FT   DOMAIN        1      8       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      9     29       POTENTIAL.
FT   DOMAIN       78    101       PORE-FORMING 1 (POTENTIAL).
FT   TRANSMEM    108    128       POTENTIAL.
FT   DOMAIN      129    158       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    159    179       POTENTIAL.
FT   DOMAIN      184    207       PORE-FORMING 2 (POTENTIAL).
FT   TRANSMEM    223    243       POTENTIAL.
FT   DOMAIN      244    394       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     53     53       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   394 AA;  43518 MW;  9FF4C8266F615FB7 CRC64;


  Query Match             12.5%;  Score 349.5;  DB 1;  Length 394;
  Best Local Similarity   32.8%;  Pred. No. 5.8e-15;
  Matches   95;  Conservative   53;  Mismatches  109;  Indels   33;  Gaps   10;

Qy      72 MKWKTV--VAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSP--- 126
           || : |  :|: |    ||: |  || |||   |  ::  : | : | ||    :|
Db       1 MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPELIERQRLELRQQE-LRARYNLSQGGY 59
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Qy    127 QELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGK 186
          :||| ::   |    |||             |    :|:|| |||||||||: ||||:|||
Db     60 EELERVVLR-LKPHKAGV----------QWRFAGSFYFAITVITTIGYGHAAPSTDGGK 107

Qy    187 IFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEK--VFRKKQVSQTKIRVISTILF 244
          :||: ||: ||||   :   :|::: |:    : | :|    |:  ||   :     :|
Db    108 VFCMFYALLGIPLTLVMFQSLGERINTLVRYLLHRAKKGLGMRRADVSMANM-----VLI 162

Qy    245 ILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVA-GGNAGINYREWYKP 303
            ||  : | |  | : | ||  :: |:  :||||:||||:||   :  :  :  |
Db    163 GFFSCISTLCIGAAAFSHYEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVA 222

Qy    304 LVWFWILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVT 353
          : :|| ||    | |:::   || ::   ::|  :     || :| :|
Db    223 FSFVYILTGLTVIGAFLNLV--VLRFMTMNAEDEKRD-----AEHRALLT 265


RESULT  14
CIW9_HUMAN
ID   CIW9_HUMAN     STANDARD;      PRT;   374 AA.
AC   Q9NPC2;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Potassium channel subfamily K member 9 (Acid-sensitive potassium
DE   channel protein TASK-3) (TWIK-related acid-sensitive K+ channel 3).
GN   KCNK9 OR TASK3.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20287530; PubMed=10747866;
RA   Rajan S., Wischmeyer E., Liu G.X., Preisig-Mueller R., Daut J.,
RA   Karschin A., Derst C.;
RT   "TASK-3, a novel tandem pore domain acid-sensitive K+ channel. An
RT   extracellular histidine as pH sensor.";
RL   J. Biol. Chem. 275:16650-16657(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Cerebellum;
RX   MEDLINE=20499203; PubMed=11042359;
RA   Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M.,
RA   Kelsell R.E., Murdock P.R., Randall A.D., Rennie G.I., Gloger I.S.;
RT   "Cloning, localisation and functional expression of a novel human,
RT   cerebellum specific, two pore domain potassium channel.";
RL   Brain Res. Mol. Brain Res. 82:74-83(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Girard C., Lesage F., Tinel N., Lazdunski M.;
RT   "Human Task-3, a novel 2P domain potassium channel related to Task.";
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Vega-Saenz de Miera E.C., Lau D.H.P., Zhadina M., Pountney D.,
RA   Coetzee W., Rudy B.;
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM
CC       CHANNEL PROTEIN.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: MAINLY FOUND IN THE CEREBELLUM.
CC   -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC       CHANNELS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF212829; AAF63708.1; -.
DR   EMBL; AF248241; AAG31730.1; -.
DR   EMBL; AF279809; AAF85982.1; -.
DR   EMBL; AF257080; AAG33126.1; -.
DR   MIM; 605874; -.
DR   InterPro; IPR003280; 2poreK_channel.
DR   InterPro; IPR000636; Cation_chan_non_lig.
DR   InterPro; IPR001622; Channel_pore_K.
DR   InterPro; IPR003092; TASK_channel.
DR   Pfam; PF00520; ion_trans; 1.
DR   PRINTS; PR01333; 2POREKCHANEL.
DR   PRINTS; PR01095; TASKCHANNEL.
KW   Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW   Glycoprotein.
FT   DOMAIN        1      8       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      9     29       POTENTIAL.
FT   DOMAIN       78    101       PORE-FORMING 1 (POTENTIAL).
FT   TRANSMEM    108    128       POTENTIAL.
FT   DOMAIN      129    158       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    159    179       POTENTIAL.
FT   DOMAIN      184    207       PORE-FORMING 2 (POTENTIAL).
FT   TRANSMEM    219    239       POTENTIAL.
FT   DOMAIN      240    374       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     53     53       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   374 AA;  42263 MW;  8A19EAEE5A4D7F38 CRC64;


  Query Match             11.9%;  Score 334;  DB 1;  Length 374;
  Best Local Similarity   28.7%;  Pred. No. 5.1e-14;
  Matches   91;  Conservative   61;  Mismatches  121;  Indels   44;  Gaps   10;

Qy     72 MKWKTV--VAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLR---------- 119
          || : |  ::: |    ||: |  || |||   |  ::  :   ||| :|
Db      1 MKRQNVRTLSLIVCTFTYLLVGAAVFDALESDHEMREEEKL---KAEEIRIKGKYNISSE 57

Qy    120 DHVCVSPQELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIA 179
          |:     ::|| :|  : :   |||          |    :|:|| |||||||||: |
Db     58 DY-----RQLELVILQS-EPHRAGV----------QWKFAGSFYFAITVITTIGYGHAA 100

Qy    180 PSTEGGKIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVI 239
          | |: || ||: ||: ||||   :   :|::: |     : |::|    :    :   ::
Db    101 PGTDAGKAFCMFYAVLGIPLTLVMFQSLGERMNTFVRYLLKRIKKCCGMRNTDVSMENMV 160

Qy    240 STILFILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAG-INYR 298
          :   |    |:  : | |  |   | |:   : |:  :||||:||||:||    | :  :
Db    161 TVGFF---SCMGTLCIGAAAFSQCEEWSFFHAYYYCFITLTTIGFGDYVALQTKGALQKK 217

Qy    299 EWYKPLVWFWILVGLAYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAA------EWKANV 352
            |   : :|||||    | |:::   || |:  :::|  : :  |:          ::
Db    218 PLYVAFSFMYILVGLTVIGAFLNLV--VLRFLTMNSEDERRDAEERASLAGNRNSMVIHI 275

Qy    353 TAEFRETRRRLSVEIHD 369
            | | :| |   :: |
Db    276 PEEPRPSRPRYKADVPD 292


RESULT  15
CIW6_HUMAN
ID   CIW6_HUMAN     STANDARD;      PRT;   313 AA.
AC   Q9Y257; Q9HB47;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Potassium channel subfamily K member 6 (Inward rectifying potassium
DE   channel protein TWIK-2) (TWIK-originated similarity sequence).
GN   KCNK6 OR TWIK2 OR TOSS.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Testis;
```

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RX   MEDLINE=99285568; PubMed=10359073;
RA   Pountney D.J., Gulkarov I., Vega-Saenz de Miera E., Holmes D.,
RA   Saganich M., Rudy B., Artman M., Coetzee W.A.;
RT   "Identification and cloning of TWIK-originated similarity sequence
RT   (TOSS): a novel human 2-pore K+ channel principal subunit.";
RL   FEBS Lett. 450:191-196(1999).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1), AND MUTAGENESIS OF CYS-53.
RC   TISSUE=Brain;
RX   MEDLINE=99175162; PubMed=10075682;
RA   Chavez R.A., Gray A.T., Zhao B.B., Kindler C.H., Mazurek M.J.,
RA   Mehta Y., Forsayeth J.R., Yost C.S.;
RT   "TWIK-2, a new weak inward rectifying member of the tandem pore domain
RT   potassium channel family.";
RL   J. Biol. Chem. 274:7887-7892(1999).
RN   [3]
RP   ERRATUM.
RA   Chavez R.A., Gray A.T., Zhao B.B., Kindler C.H., Mazurek M.J.,
RA   Mehta Y., Forsayeth J.R., Yost C.S.;
RL   J. Biol. Chem. 274:24440-24440(1999).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND CHARACTERIZATION.
RX   MEDLINE=20435832; PubMed=10887187;
RA   Patel A.J., Maingret F., Magnone V., Fosset M., Lazdunski M.,
RA   Honore E.;
RT   "TWIK-2, an inactivating 2P domain K+ channel.";
RL   J. Biol. Chem. 275:28722-28730(2000).
CC   -!- FUNCTION: Exhibits outward rectification in a physiological K(+)
CC       gradient and mild inward rectification in symmetrical K(+)
CC       conditions.
CC   -!- SUBUNIT: HOMODIMER (POTENTIAL).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
CC       produced by alternative splicing.
CC   -!- TISSUE SPECIFICITY: WIDESPREAD EXPRESSION, DETECTED IN ALL TISSUES
CC       TESTED EXCEPT FOR SKELETAL MUSCLE. STRONGEST EXPRESSION IN
CC       PLACENTA, PANCREAS, HEART, COLON AND SPLEEN, LOWER LEVELS DETECTED
CC       IN PERIPHERAL BLOOD LEUKOCYTES, LUNG, LIVER, KIDNEY AND THYMUS.
CC       LOWEST EXPRESSION DETECTED IN BRAIN.
CC   -!- MISCELLANEOUS: INHIBITED BY INTERNAL ACIDIFICATION AND, TO A SMALL
CC       DEGREE, BY ZINC. NOT INHIBITED BY QUININE, QUINIDONE OR BARIUM.
CC   -!- SIMILARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM
CC       CHANNELS.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AF134149; AAD22980.1; -.
DR   EMBL; AF117708; AAD24000.1; -.
DR   EMBL; AF281302; AAG10506.1; -.
DR   EMBL; AF281303; AAG10507.1; -.
DR   MIM; 603939; -.
DR   InterPro; IPR000636; Cation_chan_non_lig.
DR   InterPro; IPR001622; Channel_pore_K.
DR   InterPro; IPR001779; TWIK1_channel.
DR   Pfam; PF00520; ion_trans; 1.
DR   PRINTS; PR01096; TWIK1CHANNEL.
KW   Ionic channel; Transmembrane; Ion transport; Potassium transport;
KW   Glycoprotein; Alternative splicing.
FT   DOMAIN        1      4       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      5     25       POTENTIAL.
FT   DOMAIN       90    115       PORE-FORMING 1 (POTENTIAL).
FT   TRANSMEM    121    141       POTENTIAL.
FT   DOMAIN      142    172       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    173    193       POTENTIAL.
FT   DOMAIN      199    223       PORE-FORMING 2 (POTENTIAL).
FT   TRANSMEM    236    256       POTENTIAL.
FT   DOMAIN      257    313       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     79     79       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     85     85       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC      1    134       MISSING (IN ISOFORM 2).
FT   MUTAGEN      53     53       C->A: NO CHANNEL ACTIVITY.
SQ   SEQUENCE   313 AA;  33747 MW;  1379382DFB0575DE CRC64;


  Query Match             11.9%;  Score 333.5;  DB 1;  Length 313;
  Best Local Similarity   33.2%;  Pred. No. 4.4e-14;
  Matches   80;  Conservative   42;  Mismatches  108;  Indels   11;  Gaps    4;

Qy      87 YLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDADNAGVSP 146
           ||| | |:   || | |:  :  :   :|: |:   ||:   |:  ::  | |   |
Db      17 YLVLGALLVARLEGPHEARLRAELETLRAQLLQRSPCVAAPALDAFVERVLAAGRLGRVV 76

Qy     147 IGNSSNNSS----HWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLFGF 202
           : |:| :::     ||  || ||| |:|||:|||   | |: || | | :|: |:|
Db      77 LANASGSANASDPAWDFASALFFASTLITTVGYGYTTPLTDAGKAFSIAFALLGVPTTML 136

Qy     203 LLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFV--TIPAVIF 260
           ||     :|  :    :  |   :   :      |     |  | | :| |   :|||||
Db     137 LLTASAQRLSLL----LTHVPLSWLSMRWGWDPRRAACWHLVALLGVVVTVCFLVPAVIF 192

Qy     261 KYI-EGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAV 319
           :: | |: |:: ||  ::|:|:| ||:| |   |  ||  || ||  :: :||     |
Db     193 AHLEEAWSFLDAFYFCFISLSTIGLGDYVPGEAPGQPYRALYKVLVTVYLFLGLVAMVLV 252

Qy     320 L 320
           |
Db     253 L 253


Search completed: September 21, 2002, 10:00:09
Job time: 655 sec
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OM protein - protein search, using sw model

Run on:          September 21, 2002, 09:49:04 ; Search time 86.47 Seconds
                                                (without alignments)
                                                1086.345 Million cell updates/sec

Title:           US-09-729-920-2
Perfect score:   2795
Sequence:        1 MKFPIETPRKQVNWDPKVAV..........IPTDTKDREPENNSLLEDRN 543

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters:      562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       SPTREMBL_19:*
                1:  sp_archea:*
                2:  sp_bacteria:*
                3:  sp_fungi:*
                4:  sp_human:*
                5:  sp_invertebrate:*
                6:  sp_mammal:*
                7:  sp_mhc:*
                8:  sp_organelle:*
                9:  sp_phage:*
                10:  sp_plant:*
                11:  sp_rodent:*
                12:  sp_virus:*
                13:  sp_vertebrate:*
                14:  sp_unclassified:*
                15:  sp_rvirus:*
                16:  sp_bacteriap:*
                17:  sp_archeap:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1248	44.7	426	11	Q920B6	Q920b6 rattus norv
2	1243.5	44.5	370	11	Q924I4	Q924i4 rattus norv
3	1242.5	44.5	411	4	Q9NRT2	Q9nrt2 homo sapien
4	1081.5	38.7	241	11	Q9CX88	Q9cx88 mus musculu
5	860.5	30.8	248	11	Q9DA02	Q9da02 mus musculu
6	822.5	29.4	419	4	Q96T94	Q96t94 homo sapien
7	512	18.3	294	4	Q9H591	Q9h591 homo sapien
8	512	18.3	309	4	Q96T55	Q96t55 homo sapien
9	478.5	17.1	502	11	Q9JK62	Q9jk62 mus musculu
10	400	14.3	336	11	Q9Z2T2	Q9z2t2 rattus norv
11	395.5	14.2	336	11	Q99L99	Q99l99 mus musculu
12	392	14.0	332	4	Q96T54	Q96t54 homo sapien
13	389.5	13.9	343	4	Q9BXD1	Q9bxd1 homo sapien
14	382	13.7	259	6	O02821	O02821 oryctolagus
15	351.5	12.6	299	11	Q9QX34	Q9qx34 mus musculu
16	349	12.5	396	11	Q923V6	Q923v6 rattus norv
17	345.5	12.4	313	11	Q9ERU5	Q9eru5 rattus norv
18	345.5	12.4	395	11	Q9JLD4	Q9jld4 rattus norv
19	329	11.8	330	4	Q9HBC8	Q9hbc8 homo sapien
20	321	11.5	237	11	Q9ES08	Q9es08 rattus norv
21	321	11.5	330	4	Q9H427	Q9h427 homo sapien
22	316	11.3	229	4	Q9H592	Q9h592 homo sapien
23	315.5	11.3	329	5	O17185	O17185 caenorhabdi
24	312	11.2	343	11	Q9JJ14	Q9jj14 mus musculu
25	311	11.1	392	11	Q9ESM5	Q9esm5 rattus norv
26	309	11.1	398	5	Q9VFS9	Q9vfs9 drosophila
27	300.5	10.8	364	5	O76790	O76790 caenorhabdi
28	300	10.7	408	4	Q9HB14	Q9hb14 homo sapien
29	298.5	10.7	393	5	Q9XU07	Q9xu07 caenorhabdi
30	296.5	10.6	405	11	Q9ERS0	Q9ers0 rattus norv
31	295	10.6	408	4	Q96E79	Q96e79 homo sapien
32	292.5	10.5	385	5	Q9VYY5	Q9vyy5 drosophila
33	292	10.4	340	5	Q9VHE0	Q9vhe0 drosophila
34	284	10.2	430	11	Q9ERS1	Q9ers1 rattus norv
35	282.5	10.1	392	5	Q9NEV3	Q9nev3 caenorhabdi
36	282.5	10.1	411	5	Q95ZJ4	Q95zj4 caenorhabdi
37	280.5	10.0	237	11	Q920G1	Q920g1 rattus norv
38	280.5	10.0	430	4	Q9HB15	Q9hb15 homo sapien
39	268.5	9.6	522	5	Q22042	Q22042 caenorhabdi
40	264.5	9.5	444	5	O45891	O45891 caenorhabdi
41	264	9.4	551	5	Q20673	Q20673 caenorhabdi
42	264	9.4	555	5	O76789	O76789 caenorhabdi
43	262.5	9.4	443	5	O45422	O45422 caenorhabdi
44	260	9.3	461	5	Q18120	Q18120 caenorhabdi
45	258.5	9.2	513	5	Q22940	Q22940 caenorhabdi

ALIGNMENTS

```
RESULT   1
Q920B6
ID   Q920B6      PRELIMINARY;      PRT;    426 AA.
AC   Q920B6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   2P DOMAIN POTASSIUM CHANNEL KCNK2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE=21219399; PubMed=11319556;
RA   Bockenhauer D., Zilberberg N., Goldstein S.A.;
RT   "KCNK2: reversible conversion of a hippocampal potassium leak into a
RT   voltage-dependent channel.";
RL   Nat. Neurosci. 4:486-491(2001).
DR   EMBL; AF325671; AAL01159.1; -.
KW   Ionic channel.
SQ   SEQUENCE   426 AA;  46912 MW;  CACDA05BBE95FDBC CRC64;

  Query Match          44.7%;  Score 1248;  DB 11;  Length 426;
  Best Local Similarity   63.2%;  Pred. No. 8.7e-83;
  Matches  247;  Conservative   56;  Mismatches   70;  Indels   18;  Gaps    6;

Qy     16 PKVAVPAAAP-VCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMK 73
          |         ||| :  ||||          |      |||| |::  ||:| |:|  |         |||
Db     10 PGYTAGVAAPDLLDPKSA--------AQNSKPRLSFSAKPTVLASRVESDS---AINVMK 58

Qy     74 WKTVVAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLI 133
          ||||   ||:|||:||: |  ||:||||| | ||: || ::|  |:  | ||:  ||: ||
Db     59 WKTVSTIFLVVVLYLIIGATVFKALEQPQEISQRTTIVIQKQNFIAQHACVNSTELDELI 118

Qy    134 QHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYA 193
          |   : | |||: |:||:||  |||||||:||||||||||||:|||:| |||||||||:||
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```
Db    119 QQIVTAINAGIIPLGNNSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYA 178

Qy    194 IFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFV 253
          : |||||||||||:|||||||||| ||:||  | |  |||||||:||||:||| ||::||
Db    179 LLGIPLFGFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFV 238

Qy    254 TIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGL 313
           :|||||:||||:||::|||||:||||:||||:|||| : | | ::|||:|||||||||
Db    239 ALPAVIFKHIEGWSALDAIYFVVITLTTIGFGDYVAGG-SDIEYLDFYKPVVWFWILVGL 297

Qy    314 AYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQR 373
          |||||||||||||||:|||||||||| :|||||| |||||||:|||||||||:|| ||
Db    298 AYFAAVLSMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQR 357

Qy    374 AATIRSMERRRLGLDQRAHSLDMLSPEKRSV 404
          | ::   :|:|  :   :    |:| :|::
Db    358 ATSV----KRKLSAELAGNHNQELTPCRRTL 384


RESULT   2
Q924I4
ID   Q924I4      PRELIMINARY;      PRT;   370 AA.
AC   Q924I4;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MECHANOSENSITIVE TANDEM PORE POTASSIUM CHANNEL.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY;
RX   MEDLINE=21268449; PubMed=11374070;
RA   Kim Y., Bang H., Gnatenco C., Kim D.;
RT   "Synergistic interaction and the role of C-terminus in the activation
RT   of TRAAK K+ channels by pressure, free fatty acids and alkali.";
RL   Pflugers Arch. 442:64-72(2001).
DR   EMBL; AF302842; AAK60504.1; -.
KW   Ionic channel.
SQ   SEQUENCE   370 AA;  40874 MW;  54677E351CE64234 CRC64;


  Query Match             44.5%;  Score 1243.5;  DB 11;  Length 370;
  Best Local Similarity   64.0%;  Pred. No. 1.5e-82;
  Matches  245;  Conservative   54;  Mismatches   67;  Indels   17;  Gaps    5;

Qy     22 AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI 80
          ||  :  ||||        |    |||| |:: ||:| |:|  |      |||||||  |
Db      2 AAPDLLDPKSA--------AQNSKPRLSFSAKPTVLASRVESDS---AINVMKWKTVSTI 50

Qy     81 FVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD 140
          |:|||:||: |  ||:|||| | ||: || ::|  |:  | ||:  ||: |||  : |
Db     51 FLVVVLYLIIGATVFKALEQPQEISQRTTIVIQKQNFIAQHACVNSTELDELIQQIVTAI 110

Qy    141 NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF 200
          |||: |:||:||  |||||||:||||||||||:|||:| |||||||||:||: |||||
Db    111 NAGIIPLGNNSNQVSHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLF 170

Qy    201 GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF 260
          ||||||:|||||||||| ||:||  | |  |||||||:||||:||| ||::|| :|||||
Db    171 GFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIF 230

Qy    261 KYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL 320
          |:||||:||::|||||:||||:||||:|||| : | | ::|||:|||||||||||||||||
Db    231 KHIEGWSALDAIYFVVITLTTIGFGDYVAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVL 289

Qy    321 SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM 380
          |||||||||:|||||||||| :|||||| |||||||:|||||||||:|| ||| ::
Db    290 SMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSV--- 346

Qy    381 ERRRLGLDQRAHSLDMLSPEKRS 403
          :|:|  :   :    |:| |:
Db    347 -KRKLSAELAGNHNQELTPCMRT 368


RESULT   3
Q9NRT2
ID   Q9NRT2      PRELIMINARY;      PRT;   411 AA.
AC   Q9NRT2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   TWO-PORE DOMAIN POTASSIUM CHANNEL TREK-1.
GN   TREK-1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE=20244931; PubMed=10784345;
RA   Meadows H.J., Benham C.D., Cairns W., Gloger I.S., Jennings C.,
RA   Medhurst A.D., Murdock P., Chapman C.G.;
RT   "Cloning, localisation and functional expression of the human
RT   orthologue of the TREK-1 potassium channel.";
RL   Pflugers Arch. 439:714-722(2000).
DR   EMBL; AF171068; AAF89743.1; -.
DR   InterPro; IPR003280; 2poreK_channel.
DR   InterPro; IPR000636; Cation_chan_non_lig.
DR   InterPro; IPR001622; Channel_pore_K.
DR   InterPro; IPR003976; Trek_channel.
DR   Pfam; PF00520; ion_trans; 1.
DR   PRINTS; PR01333; 2POREKCHANEL.
DR   PRINTS; PR01499; TREKCHANNEL.
KW   Ionic channel.
SQ   SEQUENCE   411 AA;  45494 MW;  FDE40CAB21B42A1C CRC64;


  Query Match             44.5%;  Score 1242.5;  DB 4;  Length 411;
  Best Local Similarity   63.5%;  Pred. No. 2.1e-82;
  Matches  244;  Conservative   57;  Mismatches   66;  Indels   17;  Gaps    5;

Qy     22 AAAPVCQPKSATNGQPPAPAPTPTPRLSISSRATVVA-RMEGTSQGGLQTVMKWKTVVAI 80
          ||  :  ||||        |    |||| |:: ||:| |:|  |      |||||||  |
Db      2 AAPDLLDPKSA--------AQNSKPRLSFSTKPTVLASRVESDT---TINVMKWKTVSTI 50

Qy     81 FVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDAD 140
          |:|||:||: |  ||:|||| | ||: || ::|  |:  | ||:  ||: |||  : |
Db     51 FLVVVLYLIIGATVFKALEQPHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIVAAI 110

Qy    141 NAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLF 200
          |||: |:||:||  |||||||:||||||||||:|||:| |||||||||:||: |||||
Db    111 NAGIIPLGNTSNQISHWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLF 170

Qy    201 GFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIF 260
          ||||||:|||||||||| ||:||  | |  |||||||:||||:||| ||::|| :|||||
Db    171 GFLLAGVGDQLGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIIFILFGCVLFVALPAIIF 230

Qy    261 KYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVL 320
          |:||||:||::|||||:||||:||||:|||| : | | ::|||:|||||||||||||||||
Db    231 KHIEGWSALDAIYFVVITLTTIGFGDYVAGG-SDIEYLDFYKPVVWFWILVGLAYFAAVL 289

Qy    321 SMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSM 380
          |||||||||:|||||||||| :|||||| |||||||:|||||||||:|| ||| :|
Db    290 SMIGDWLRVISKKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSI--- 346

Qy    381 ERRRLGLDQRAHSLDMLSPEKRSV 404
          :|:|  :   :    |:| :|::
Db    347 -KRKLSAELAGNHNQELTPCRRTL 369


RESULT   4
Q9CX88
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ID   Q9CX88      PRELIMINARY;      PRT;   241 AA.
AC   Q9CX88;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   3010005K24RIK PROTEIN.
GN   3010005K24RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=EMBRYONIC HEAD;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK019376; BAB31686.1; -.
DR   MGD; MGI:1924704; 3010005K24Rik.
DR   InterPro; IPR001622; Channel_pore_K.
SQ   SEQUENCE   241 AA;  25799 MW;  B4C39F77CD0A39DA CRC64;
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  Query Match             38.7%;  Score 1081.5;  DB 11;  Length 241;
  Best Local Similarity   93.9%;  Pred. No. 5.3e-71;
  Matches  214;  Conservative    3;  Mismatches    4;  Indels    7;  Gaps    2;

Qy       1 MKFPIETPRKQVNWDPKVAVPAAA-PVCQPKSATNGQPPAPAPTPTPRLSISSRATVVAR 59
           |||||||||||||||||||||||| |||||||||||        | ||||||||||||||
Db       1 MKFPIETPRKQVNWDPKVAVPAAAPPVCQPKSATNGH------HPVPRLSISSRATVVAR 54

Qy      60 MEGTSQGGLQTVMKWKTVVAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLR 119
           ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      55 MEGASQGGLQTVMKWKTVVAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLR 114

Qy     120 DHVCVSPQELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIA 179
           ||:|||||||||||||||||||||:|||||:|||||||||||||||||||||||||||||||
Db     115 DHICVSPQELETLIQHALDADNAGVSPVGNSSNSSSHWDLGSAFFFAGTVITTIGYGNIA 174

Qy     180 PSTEGGKIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFR 227
           ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     175 PSTEGGKIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFR 222
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RESULT   5
Q9DA02
ID   Q9DA02      PRELIMINARY;      PRT;   248 AA.
AC   Q9DA02;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   1700024D23RIK PROTEIN.
GN   1700024D23RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=TESTIS;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK006295; BAB24513.1; -.
DR   MGD; MGI:1919508; 1700024D23Rik.
DR   InterPro; IPR000636; Cation_chan_non_lig.
DR   InterPro; IPR001622; Channel_pore_K.
DR   Pfam; PF00520; ion_trans; 1.
SQ   SEQUENCE   248 AA;  27233 MW;  9C45EC1B09E3AEA7 CRC64;
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  Query Match             30.8%;  Score 860.5;  DB 11;  Length 248;
  Best Local Similarity   91.5%;  Pred. No. 6.8e-55;
  Matches  172;  Conservative    4;  Mismatches    5;  Indels    7;  Gaps    2;

Qy      18 VAVPAAA-PVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKT 76
           ||||||| |||||||||||        | ||||||||||||||| ||||||||||||
Db      28 VAVPAAAPPVCQPKSATNGH------HPVPRLSISSRATVVARMEGASQGGLQTVMKWKT 81

Qy      77 VVAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHA 136
           |||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db      82 VVAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHICVSPQELETLIQHA 141

Qy     137 LDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFG 196
           ||||||||||:|||||:||||||||||||||||||||||||||||||||||||||||||||
Db     142 LDADNAGVSPVGNSSNSSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFG 201

Qy     197 IPLFGFLL 204
           |||| ||:
Db     202 IPLFWFLI 209
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RESULT   6
Q96T94
ID   Q96T94      PRELIMINARY;      PRT;   419 AA.
AC   Q96T94;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   TWO PORE K+ CHANNEL KT4.1B.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ozaita A., Vega-Saenz de Miera E.C.;
RT   "Cloning of Two transcripts of the Human 2-Pore K+ channel KT4.1 Gene.
RT   Chromosomal Localization, Tissue Distribution and Functional
RT   Expression.";
```

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RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF259501; AAK49390.1; -.
KW   Ionic channel.
SQ   SEQUENCE   419 AA;  45173 MW;  E7DEDE17B30C0FBF CRC64;


  Query Match             29.4%;  Score 822.5;  DB 4;  Length 419;
  Best Local Similarity   48.4%;  Pred. No. 8.1e-52;
  Matches  164;  Conservative   55;  Mismatches   87;  Indels   33;  Gaps   4;

Qy      25 PVCQPKSATNGQPPAPAPTPTPRLSISSRATVVARMEGTSQGGLQTVMKWKTVVAIFVVV 84
           |  :|  | :|  |||                                 |:  |::|:  :|
Db       8 PPARPLQAGSGAGPAPG----------------------------RAMRSTTLLALLALV 39

Qy      85 VVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDADNAGV 144
           ::|||:| |||||||| |   :  :   : :||| | ||| |||  ||:   ||   |
Db      40 LLYLVSGALVFRALEQPHEQQAQRELGEVREKFLRAHPCVSDQELGLLIKEVADALGGGA 99

Qy     145 SPIGNSSNNSSH--WDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLFGF 202
           |  ||::|||  |||||||||:||:||||||||:|  |: |::||| ||: ||||||
Db     100 DPETNSTSNSSHSAWDLGSAFFFSGTIITTIGYGNVALRTDAGRLFCIFYALVGIPLFGI 159

Qy     203 LLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIFKY 262
           ||||:||:||:     |  :| :| |  |    :||:| :||:| ||::||  |  :| |
Db     160 LLAGVGDRLGSSLRHGIGHIEAIFLKWHVPPELVRVLSAMLFLLIGCLLFVLTPTFVFCY 219

Qy     263 IEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVLSM 322
           :| |: ||:||||:||||||||||:||| :   :    |:||||||||:||||||:||:
Db     220 MEDWSKLEAIYFVIVTLTTVGFGDYVAGADPRQD-SPAYQPLVWFWILLGLAYFASVLTT 278

Qy     323 IGDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRR 361
           ||:||||:|::|: |:| : | || |   |||  | |:|
Db     279 IGNWLRVVSRRTRAEMGGLTAQAASWTGTVTA--RVTQR 315


RESULT   7
Q9H591
ID   Q9H591      PRELIMINARY;      PRT;   294 AA.
AC   Q9H591;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   DJ137F1.2 (NOVEL MEMBER OF THE POTASSIUM CHANNEL SUBFAMILY K).
GN   DJ137F1.2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Williams S.;
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL136087; CAC07336.1; -.
DR   InterPro; IPR003280; 2poreK_channel.
DR   InterPro; IPR000636; Cation_chan_non_lig.
DR   InterPro; IPR001622; Channel_pore_K.
DR   Pfam; PF00520; ion_trans; 1.
DR   PRINTS; PR01333; 2POREKCHANEL.
KW   Ionic channel.
SQ   SEQUENCE   294 AA;  32507 MW;  FCBA3B352F1F0952 CRC64;


  Query Match             18.3%;  Score 512;  DB 4;  Length 294;
  Best Local Similarity   40.2%;  Pred. No. 2e-29;
  Matches   99;  Conservative   55;  Mismatches   86;  Indels    6;  Gaps    3;

Qy      77 VVAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHA 136
           |: : :  | ||: |  :|: ||:  |:  ::   |||  || :: |:    :|  :|
Db      14 VLPLLLAYVCYLLLGATIFQLLERQAEAQSRDQFQLEKLRFLENYTCLDQWAMEQFVQVI 73

Qy     137 LDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFG 196
           ::|   ||:| |||: | |:|| ||:|||||||:|||||||:|||||  |::||: ||: |
Db      74 MEAWVKGVNPKGNST-NPSNWDFGSSFFFAGTVVTTIGYGNLAPSTEAGQVFCVFYALLG 132

Qy     197 IPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIP 256
           |||    |    : |||     :| :|:   : : ||  ::|:   ||:  | :| :  |
Db     133 IPLNVIFL----NHLGTGLRAHLAAIERWEDRPRRSQV-LQVLGLALFLTLGTLVILIFP 187

Qy     257 AVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYF 316
           ::| ::|||:  |  ||  :||:|:||||:| | :   :|   |: |   |||:|||:
Db     188 PMVFSHVEGWSFSEGFYFAFITLSTIGFGDYVVGTDPSKHYISVYRSLAAIWILLGLAWL 247

Qy     317 AAVLSM 322
           | :| :
Db     248 ALILPL 253


RESULT   8
Q96T55
ID   Q96T55      PRELIMINARY;      PRT;   309 AA.
AC   Q96T55;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   2P DOMAIN POTASSIUM CHANNEL TALK-1.
GN   KCNK16.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Girard C., Duprat F., Terrenoire C., Tinel N., Fosset M., Romey G.,
RA   Lazdunski M., Lesage F.;
RT   "Genomic and functional characteristics of novel human pancreatic 2P
RT   domain K+ channels.";
RL   Biochem. Biophys. Res. Commun. 0:0-0(2001).
DR   EMBL; AF358909; AAK49532.1; -.
KW   Ionic channel.
SQ   SEQUENCE   309 AA;  34153 MW;  99C4B11EB26B0764 CRC64;


  Query Match             18.3%;  Score 512;  DB 4;  Length 309;
  Best Local Similarity   40.2%;  Pred. No. 2.2e-29;
  Matches   99;  Conservative   55;  Mismatches   86;  Indels    6;  Gaps    3;

Qy      77 VVAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHA 136
           |: : :  | ||: |  :|: ||:  |:  ::   |||  || :: |:    :|  :|
Db      14 VLPLLLAYVCYLLLGATIFQLLERQAEAQSRDQFQLEKLRFLENYTCLDQWAMEQFVQVI 73

Qy     137 LDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFG 196
           ::|   ||:| |||: | |:|| ||:|||||||:|||||||:|||||  |::||: ||: |
Db      74 MEAWVKGVNPKGNST-NPSNWDFGSSFFFAGTVVTTIGYGNLAPSTEAGQVFCVFYALLG 132

Qy     197 IPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIP 256
           |||    |    : |||     :| :|:   : : ||  ::|:   ||:  | :| :  |
Db     133 IPLNVIFL----NHLGTGLRAHLAAIERWEDRPRRSQV-LQVLGLALFLTLGTLVILIFP 187

Qy     257 AVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYF 316
           ::| ::|||:  |  ||  :||:|:||||:| | :   :|   |: |   |||:|||:
Db     188 PMVFSHVEGWSFSEGFYFAFITLSTIGFGDYVVGTDPSKHYISVYRSLAAIWILLGLAWL 247

Qy     317 AAVLSM 322
           | :| :
Db     248 ALILPL 253


RESULT   9
Q9JK62
ID   Q9JK62      PRELIMINARY;      PRT;   502 AA.
AC   Q9JK62;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   POTASSIUM CHANNEL TASK2 (TASK2 POTASSIUM CHANNEL).
GN   KCNK5.
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```
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=129/SVJ; TISSUE=KIDNEY;
RA   Roux J., Barhanin J.;
RT   "Mouse two P domain potassium channel TASK2.";
RL   Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=KIDNEY;
RA   Cid L.P., Niemeyer M.I., Sepulveda F.V.;
RT   "Functional properties of mouse TASK-2 potassium channel.";
RL   Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF259395; AAF68668.1; -.
DR   EMBL; AF319542; AAG35065.1; -.
DR   MGD; MGI:1336175; Kcnk5.
DR   InterPro; IPR003280; 2poreK_channel.
DR   InterPro; IPR000636; Cation_chan_non_lig.
DR   InterPro; IPR001622; Channel_pore_K.
DR   Pfam; PF00520; ion_trans; 1.
DR   PRINTS; PR01333; 2POREKCHANEL.
KW   Ionic channel.
SQ   SEQUENCE   502 AA;  55976 MW;  E4C7E7CC71B44D95 CRC64;

  Query Match             17.1%;  Score 478.5;  DB 11;  Length 502;
  Best Local Similarity   27.0%;  Pred. No. 1.1e-26;
  Matches  126;  Conservative   76;  Mismatches  185;  Indels   79;  Gaps   13;

Qy      84 VVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALDADNAG 143
           ::.||  |  :|  ||:|     |    :|   |::  |:| : |: ::|   || : |
Db      12 IIFYLAIGAAIFEVLEEPHWKEAKKNYYTQKLHLLKEFPCLSQEGLDKILQVVSDAADQG 71

Qy     144 VSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIPLFGFL 203
           |:  || : |  :|:  :|  || |||||||||:|| |  |::||: | :||:||
Db      72 VAITGNQTFN--NWNWPNAMIFAATVITTIGYGNVAPKTPAGRLFCVFYGLFGVPL---C 126

Qy     204 LAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVTIPAVIFKYI 263
           |  |   ||  ||    |: :   :: ||  | ::  | :||: | :| : ||  :|
Db     127 LTWI-SALGKFFGGRAKRLGQFLTRRGVSLRKAQITCTAIFIVWGVLVHLVIPPFVFMVT 185

Qy     264 EGWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFWILVGLAYFAAVLSMI 323
           | |  :| :|:  :|:::|:|||||||| |   ||   |:  |  || :|||
Db     186 EEWNYIEGLYYSFITISTIGFGDFVAGVNPSANYHALYRYFVELWIYLGLA--------- 236

Qy     324 GDWLRVLSKKTKEEVGEIKAHAAEWKANVTAEFRETRRRLSVEIHDKLQRAATIRSMERR 383
             || :           || :           : ||:|  ::     :   ||
Db     237 --WLSLF---------------VNWKVS----------MFVEVHKAIK-----KRRRRR 263

Qy     384 RLGLDQRAHSLDMLSPEKRSVFAALDTGRFKASSQESINNRPNNL------------RLK 431
           :   :   ||   |     :    ::   | :  :|: |:    :             |:
Db     264 KESFESSPHSRKALQMAGSTASKDVNIFSFLSKKEETYNDLIKQIGKKAMKTSGGGERVP 323

Qy     432 GPEQLNKHGQGASEDNIINKFGSTSRLTKRKNKDLKKTLPEDVQKIYKTFRNYSLDEEKK 491
           ||     || |   | :     | : |         |  :|  :::: :| :|
Db     324 GP----GHGLGPQGDRLPTIPASLAPLVVYS---KNRVP-SLEEVSQTLKNKGHVSRPL 374

Qy     492 EEETEKMCNSDNSSTAML----TDCIQQHAELENGMIPTDTKDREP 533
           ||       |:  |: :     | | :  |      | :  |  |
Db     375 GEEAGAQAPKDSYQTSEVFINQLDRISEEGE------PWEALDYHP 414


RESULT  10
Q9Z2T2
ID   Q9Z2T2      PRELIMINARY;      PRT;   336 AA.
AC   Q9Z2T2;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   PUTATIVE POTASSIUM CHANNEL TWIK.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Gan L., Joiner W.J., Quinn A.M., Wang L.-Y., Hughes T.,
RA   Kaczmarek L.K.;
RT   "Cloning and localization of rTWIK, a putative potassium channel with
RT   two P domains.";
RL   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF022819; AAD09336.1; -.
DR   InterPro; IPR003280; 2poreK_channel.
DR   InterPro; IPR000636; Cation_chan_non_lig.
DR   InterPro; IPR001622; Channel_pore_K.
DR   InterPro; IPR001779; TWIK1_channel.
DR   Pfam; PF00520; ion_trans; 1.
DR   PRINTS; PR01333; 2POREKCHANEL.
DR   PRINTS; PR01096; TWIK1CHANNEL.
KW   Ionic channel.
SQ   SEQUENCE   336 AA;  38228 MW;  5E78031947D75DE6 CRC64;

  Query Match             14.3%;  Score 400;  DB 11;  Length 336;
  Best Local Similarity   30.5%;  Pred. No. 3.4e-21;
  Matches  100;  Conservative   60;  Mismatches  108;  Indels   60;  Gaps   11;

Qy      81 FVVV--VVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALD 138
           |:|:  ::||| | :|| ::| |:|   :  :   |  || :| |:|  :||  :   |:
Db      25 FLVLGYLLYLVFGAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEPQLEQFLGRVLE 84

Qy     139 ADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIP 198
           | | ||| : |:| |  :||  || ||| ||::| |||:  | ::||| |||:|:: |||
Db      85 ASNYGVSVLSNASGN-WNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIP 143

Qy     199 LFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQV---------SQTKIRVISTIL--FILA 247
             |  :           : ||     :: |           |:  : ::  :|  |:
Db     144 FTLLFLTAV-----------VQRVTVHVTRRPVLYFHIRWGFSKQVVAIVHAVLLGFVTV 192

Qy     248 GCIVFVTIPAVIFKYIE-GWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVW 306
           |  |  ||| :|  :|  |  ||| ||  ::|:|:| ||:| |      :|| ||  :
Db     193 SCFFF--IPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYKIGIT 250

Qy     307 FWILVGLAYFAAVLSMIGDWLRVLSK-----KTKEEVGEIKAHAAEWKANVTAEFRETRR 361
           ::|:||     ||    : |  | |       |::  | : |  |
Db     251 CYLLLGLIAMLVVLETFCE-LHELKKFRKMFYVKKDKDEDQVHIME-------------- 295

Qy     362 RLSVEIHDKL------QRAATIRSMERR 383
             ||:|      ::|| ::  :::
Db     296 ------HDQLSFSSITEQAAGLKEEQKQ 317


RESULT  11
Q99L99
ID   Q99L99      PRELIMINARY;      PRT;   336 AA.
AC   Q99L99;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   POTASSIUM CHANNEL, SUBFAMILY K, MEMBER 1.
GN   KCNK1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC003729; AAH03729.1; -.
DR   MGD; MGI:109322; Kcnk1.
DR   InterPro; IPR003280; 2poreK_channel.
DR   InterPro; IPR000636; Cation_chan_non_lig.
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DR   InterPro; IPR001622; Channel_pore_K.
DR   InterPro; IPR001779; TWIK1_channel.
DR   Pfam; PF00520; ion_trans; 1.
DR   PRINTS; PR01333; 2POREKCHANEL.
DR   PRINTS; PR01096; TWIK1CHANNEL.
SQ   SEQUENCE   336 AA;  38201 MW;  76B7FD5361A6216C CRC64;


  Query Match             14.2%;  Score 395.5;  DB 11;  Length 336;
  Best Local Similarity   33.7%;  Pred. No. 7.3e-21;
  Matches   94;  Conservative   50;  Mismatches   98;  Indels   37;  Gaps    9;

Qy      81 FVVV--VVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALD 138
           |:|:  ::||| | :|| ::| |:|   :  :   |  || :| |:|  :||  :   |:
Db      25 FLVLGYLLYLVFGAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEPQLEQFLGRVLE 84

Qy     139 ADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIP 198
           | | ||| : |:| |  :||  || ||| ||::| |||:  | ::||| |||:|:: |||
Db      85 ASNYGVSVLSNASGN-WNWDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIP 143

Qy     199 LFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQV---------SQTKIRVISTIL--FILA 247
                 |  :          : ||     :: |         |:  : ::  :|  |:
Db     144 FTLLFLTAV-----------VQRVTVHVTRRPVLYFHIRWGFSKQVVAIVHAVLLGFVTV 192

Qy     248 GCIVFVTIPAVIFKYIE-GWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVW 306
           |  |  ||| :|  :|  |  ||| ||  ::|:|:| ||:|  |      :|| ||  :
Db     193 SCFFF--IPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYKIGIT 250

Qy     307 FWILVGLAYFAAVLSMIGDWLRVLS--------KKTKEE 337
            ::|:||     ||    : |  |          || |:|
Db     251 CYLLLGLIAMLVVLETFCE-LHELKKFRKMFYVKKDKDE 288


RESULT  12
Q96T54
ID   Q96T54      PRELIMINARY;      PRT;   332 AA.
AC   Q96T54;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   2P DOMAIN POTASSIUM CHANNEL TALK-2.
GN   KCNK17.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Girard C., Duprat F., Terrenoire C., Tinel N., Fosset M., Romey G.,
RA   Lazdunski M., Lesage F.;
RT   "Genomic and functional characteristics of novel human pancreatic 2P
RT   domain K+ channels.";
RL   Biochem. Biophys. Res. Commun. 0:0-0(2001).
DR   EMBL; AF358910; AAK49533.1; -.
KW   Ionic channel.
SQ   SEQUENCE   332 AA;  36894 MW;  1848DBC06E078158 CRC64;


  Query Match             14.0%;  Score 392;  DB 4;  Length 332;
  Best Local Similarity   31.2%;  Pred. No. 1.3e-20;
  Matches   85;  Conservative   59;  Mismatches  114;  Indels   14;  Gaps    3;

Qy      52 SRATVVARMEGTSQGGLQTVMKWKTVVAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIA 111
           :||    |: | :          : | :  :  : ||  |  ||  ||          :
Db       6 ARAAPEGRVRGCAV---------PSTVLLLLAYLAYLALGTGVFWTLEGRAAQDSSRSFQ 56

Qy     112 LEKAEFLRDHVCVSPQELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVIT 171
           :| | |::  |:    |::||:  : |   | | : |:: :   |:|  :|||: : ||
Db      57 RDKWELLQNFTCLDRPALDSLIRDVVQAYKNGASLLSNTT-SMGRWELVGSFFFSVSTIT 115

Qy     172 TIGYGNIAPSTEGGKIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQV 231
           ||||||::|:|   ::||| :|: ||||   :|    ::|| :  : :
Db     116 TIGYGNLSPNTMAARLFCIFFALVGIPLNLVVL----NRLGHLMQQGVNHWASRLGGTWQ 171

Qy     232 SQTKIRVISTILFILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGG 291
           | | ::    :|:| ::|: :| ::| ::|||:  |  ||  :||:||||||:| |
Db     172 DPDKARWLAGSGALLSGLLLFLLLPPLLFSHMEGWSYTEGFYFAFITLSTVGFGDYVIGM 231

Qy     292 NAGINYREWYKPLVWFWILVGLAYFAAVLSMI 323
           |    |  ||| :|  ||| |:|: | :: :|
Db     232 NPSQRYPLWYKNMVSLWILFGMAWLALIIKLI 263


RESULT  13
Q9BXD1
ID   Q9BXD1      PRELIMINARY;      PRT;   343 AA.
AC   Q9BXD1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   POTASSIUM CHANNEL TASK-4.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=ADRENAL GLAND;
RX   MEDLINE=21145510; PubMed=11248242;
RA   Decher N., Maier M., Dittrich W., Gassenhuber J., Bruggemann A.,
RA   Busch A.E., Steinmeyer K.;
RT   "Characterization of TASK-4, a novel member of the pH-sensitive, two-
RT   pore domain potassium channel family.";
RL   FEBS Lett. 492:84-89(2001).
DR   EMBL; AF339912; AAK28551.1; -.
DR   InterPro; IPR003280; 2poreK_channel.
DR   InterPro; IPR000636; Cation_chan_non_lig.
DR   InterPro; IPR001622; Channel_pore_K.
DR   Pfam; PF00520; ion_trans; 1.
DR   PRINTS; PR01333; 2POREKCHANEL.
SQ   SEQUENCE   343 AA;  38172 MW;  29B1F354CE22E3BB CRC64;


  Query Match             13.9%;  Score 389.5;  DB 4;  Length 343;
  Best Local Similarity   30.3%;  Pred. No. 2.1e-20;
  Matches   91;  Conservative   59;  Mismatches  125;  Indels   25;  Gaps    5;

Qy      52 SRATVVARMEGTSQGGLQTVMKWKTVVAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIA 111
           :||    |: | :  |          | : :  : ||  |  ||  ||          :
Db       6 ARAAPEGRVRGCAVPG---------TVLLLLAYLAYLALGTGVFWTLEGRAAQDSSRSFQ 56

Qy     112 LEKAEFLRDHVCVSPQELETLIQHALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVIT 171
           :| | |::  |:    |::||:  : |   | | : |:: :   |:|  :|||: : ||
Db      57 RDKWELLQNFTCLDRPALDSLIRDVVQAYKNGASLLSNTT-SMGRWELVGSFFFSVSTIT 115

Qy     172 TIGYGNIAPSTEGGKIFCILYAIFGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQV 231
           ||||||::|:|   ::||| :|: ||||   :|    ::|| :  : :
Db     116 TIGYGNLSPNTMAARLFCIFFALVGIPLNLVVL----NRLGHLMQQGVNHWASRLGGTWQ 171

Qy     232 SQTKIRVISTILFILAGCIVFVTIPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVAGG 291
           | | ::    :|:| ::|: :| ::| ::|||:  |  ||  :||:||||||:| |
Db     172 DPDKARWLAGSGALLSGLLLFLLLPPLLFSHMEGWSYTEGFYFAFITLSTVGFGDYVIGM 231

Qy     292 NAGINYREWYKPLVWFWILVGLAYFAAVL-SMIGDWLR----------VLSKKTKEEVGE 340
           |    |  ||| :|  ||| |:|: | :  |    | |           | | :  : |:
Db     232 NPSQRYPLWYKNMVSLWILFGMAWLALISNSSSPSWRRQGGYVPAATTALRKTSSPKAGD 291


RESULT  14
O02821
ID   O02821      PRELIMINARY;      PRT;   259 AA.
AC   O02821;
DT   01-JUL-1997 (TrEMBLrel. 04, Created)
DT   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   RABKCNK1 (FRAGMENT).
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OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Orias M., Velazquez H., Tung F., Desir G.V.;
RT   "Cloning and nephron segment localization of a double pore K channel,
RT   KCNK1: exclusive distal expression.";
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF004695; AAB61602.1; -.
DR   InterPro; IPR003280; 2poreK_channel.
DR   InterPro; IPR000636; Cation_chan_non_lig.
DR   InterPro; IPR001622; Channel_pore_K.
DR   InterPro; IPR001779; TWIK1_channel.
DR   Pfam; PF00520; ion_trans; 1.
DR   PRINTS; PR01333; 2POREKCHANEL.
DR   PRINTS; PR01096; TWIK1CHANNEL.
FT   NON_TER       1      1
FT   NON_TER     259    259
SQ   SEQUENCE   259 AA;  29311 MW;  5546A8BD278E79F3 CRC64;


  Query Match             13.7%;  Score 382;  DB 6;  Length 259;
  Best Local Similarity   35.1%;  Pred. No. 4.9e-20;
  Matches   86;  Conservative   48;  Mismatches   87;  Indels   24;  Gaps    6;

Qy      81 FVVV--VVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSPQELETLIQHALD 138
           |:|:  ::|||  | :|| ::| |:|   :  :   |  |: :| |:| |:||  :   |:
Db      26 FLVLGYLLYLVFGAVVFSSVELPYEDLLRQELRKLKRRFVEEHECLSEQQLEQFLGRVLE 85

Qy     139 ADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAIFGIP 198
           |:| |||   |:| |  :||  || ||| ||::| |||:  | :: || |||:|:: |||
Db      86 ANNYGVSVRSNASGN-WNWDFASALFFASTVLSTTGYGHTVPLSDVGKAFCIIYSVIGIP 144

Qy     199 LFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIR------VISTILFILAGCIV- 251
               |  :          : ||     :: |    :|      |:: :  :| | |
Db     145 FTLLFLTAV----------VQRVTVHVTRRPVLYFHVRWGFSKQVVAIVHAVLLGLITV 193

Qy     252 --FVTIPAVIFKYIE-GWTALESIYFVVVTLTTVGFGDFVAGGNAGINYREWYKPLVWFW 308
             |  ||| :|  :|  |  ||| ||  ::|:|:| ||:| |      :|| ||  :  :
Db     194 SCFFFIPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPGEGYNQKFRELYKIGITCY 253

Qy     309 ILVGL 313
           :|:||
Db     254 LLLGL 258


RESULT  15
Q9QX34
ID   Q9QX34      PRELIMINARY;      PRT;   299 AA.
AC   Q9QX34;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   PUTATIVE POTASSIUM CHANNEL DP4 (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Gan L., Joiner W.J., Quinn A.M., Wang L.-Y., Hughes T.,
RA   Kaczmarek L.K.;
RL   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF022821; AAD09338.1; -.
DR   InterPro; IPR003280; 2poreK_channel.
DR   InterPro; IPR000636; Cation_chan_non_lig.
DR   InterPro; IPR001622; Channel_pore_K.
DR   InterPro; IPR003092; TASK_channel.
DR   Pfam; PF00520; ion_trans; 1.
DR   PRINTS; PR01333; 2POREKCHANEL.
DR   PRINTS; PR01095; TASKCHANNEL.
KW   Ionic channel.
FT   NON_TER       1      1
FT   NON_TER     299    299
SQ   SEQUENCE   299 AA;  33325 MW;  DCD41D8A212939C4 CRC64;


  Query Match             12.6%;  Score 351.5;  DB 11;  Length 299;
  Best Local Similarity   32.1%;  Pred. No. 1e-17;
  Matches   90;  Conservative   53;  Mismatches  110;  Indels   27;  Gaps    8;

Qy      78 VAIFVVVVVYLVTGGLVFRALEQPFESSQKNTIALEKAEFLRDHVCVSP---QELETLIQ 134
           :|: |    ||: |  || |||   |  ::  : | : | ||    :|    :||| ::
Db       7 LALIVCTFTYLLVGAAVFDALESEPEMIERQRLELRQLE-LRARYNLSEGGYEELERVVL 65

Qy     135 HALDADNAGVSPIGNSSNNSSHWDLGSAFFFAGTVITTIGYGNIAPSTEGGKIFCILYAI 194
             |   |||           |    :|:|| |||||||||: ||||:|||:||: ||:
Db      66 R-LKPHKAGV-----------QWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFCMFYAL 113

Qy     195 FGIPLFGFLLAGIGDQLGTIFGKSIARVEKVFRKKQVSQTKIRVISTILFILAGCIVFVT 254
           ||||   :   :|::: |     : | :   |   :   :: : : :|     ||  :
Db     114 LGIPLTLVMFQSLGERINTFVRYLLHRAK---RGLGMRHAEVSMANMVLIGFVSCISTLC 170

Qy     255 IPAVIFKYIEGWTALESIYFVVVTLTTVGFGDFVA-GGNAGINYREWYKPLVWFWILVGL 313
           | |  | | | ||  :: |:  :||||:||||:||   :  :  :  |    : :|| ||
Db     171 IGAAAFSYYERWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTQPQYVAFSFVYILTGL 230

Qy     314 AYFAAVLSMIGDWLRVLSKKTKEEVGEIKAHAAEWKANVT 353
             | |:::   || ::   ::|  :     || :| :|
Db     231 TVIGAFLNLV--VLRFMTMNAEDEKRD-----AEHRALLT 263


Search completed: September 21, 2002, 09:59:18
Job time: 614 sec
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